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Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/abss/ABSSWEB spool/US09611257/runat 10072006 064126 6972/app query.fasta.1
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXIEN=2000000000 -HOST=abss06p
-USER=US09611257 @CGN 1 1 7492 @runat 10072006 064126 6972 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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US-10-377-139-7

US-10-377-139-7

Sequence 7, Application US/10377139

Publication No. US20040175761A1

Sequence 7, Application US/10377139

Publication No. US20040175761A1

SEQUENCE 1 INFORMATION:

SAPLICANT: Diag, Youxing

APPLICANT: Lee MacKinnon, Alice

APPLICANT: Lee MacKinnon, Alice

APPLICANT: Lee MacKinnon, Alice

APPLICANT: Buta, Vanessa

TITLE OF INVENTION: Uses Thereof

TITLE OF INVENTION:
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Sequence 3, Application US/09383894
Sequence 3, Application US/09383894
Publication No. US20030125269A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: T-Type Calcium Channel
FILE REFERENCE: 004.00191
CURRENT APPLICATION NUMBER: US/09/383,894
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,004
EARLIER FILING DATE: 1998-08-26
EARLIER FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 7285
TYPE: DNA
CORGANISM: Rattus Sp.
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US-09-383-894-1
; Sequence 1, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
   APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT APPLICATION NUMBER: US 60/098,004
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER PILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 1
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; LENGTH: 7129
; ORGANISM: Rattus sp.
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; Publication No. US2005
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nata
APPLICANT: Zlotnik,
; TITLE OF INVENTION:
; FILE REFERENCE: file
; CURRENT APPLICATION N
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; CURRENT FILING DATE:
; NUMBER OF SEQ ID NOS:
; SOFTWARE: Patentin ve;
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LENGTH: 7825
; TYPE: DNA
; ORGANISM: Homo Sapie
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PTYTHISALAASPCYSHISLeuGluProValArgCYSGlnA athrGlnAspAlaGlnHisSerAspLeuArgAspProHisS JG1UI1eSerAsnI1eValPheThrSerLeuPheAlaLeuG 1ValValLeuMetLysThrMetAspAsnValAlaThrPheC

	4355 AGGTGGTGGCTGGTGCTTCGGGGGAGCGGCGTACCTGCGGAGCAGCTTGGA 1359 alLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValS 4415 TGCTGGACGGCTGTTGGTGCTCATCTCGTCATCGACATTCTGGTGTCCATGGTCT 1379 spSexGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuA 4475 ACAGCGGCACCAAGATCCTGGGCATGCTGAGGTGCTGCGGCCCTGC	99 roLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMe 	GIyLysPhePheValCysGl 	79 snPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLy	19 snHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaF 	59 luGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysLys	roTyrTyrSerAspTyrSerArgP]
942 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 962		98 GCCTGGATGGTGATGGGACAGGAAGAGTGCTTGGCCTTGGTGCCCTGGGAGGCACC 39 laGluLeuArgLysSerLeuLeuProProLeuIleIleHisThralaAlaThrProMetS 6	079 hrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisHisGluMetLysCysProProS 109	119 erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA 113	159 luAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA 117	199 erGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL 121 [239 lyAsnLeuSerLysGlyGluArglleGlnAlaTrpValArgSerArgLeuProAlaCysC 125
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hrvalt 1339 |||||| CAGTGA 4354 rpAsnV 1359 |||||| GGAACG 4414 alserA 1379 ||||||| |CTCTG 4474 euArgP 1399 |||||| |GCGCC 4534 etSerS 1419 |||||| TGTCCT 4594 hrarga 1459 |||||| |CCAGGA 4714 spGlyT 1499 |||||||| ATGGTT 4834 leMeta 1519 |||||| |CATGA 4894 hePheV 1539 ||||||| TCTTTG 4954 ysarga 1579 ||||||| agagaa 5074 isLeuC 1608 ||||||| ACTTGT 5194 luargi 1319 |||||| qacgca 4294 laGluA 1588 ::|||| CAGAAG 5134 heGlyI 1439 |||||| TCGGCA 4654 isGlnG 1559 |||||| ACCAGG 5014 alThrM 1628 |||||| |CACCA 5254 '8AsnT 1648

qq	55 TGGCCATGGAGCACTACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACT 531	δ	1928
දු දු	1648 yrilePheThrValilePheValPheGluSerValPheLysLeuValAlaPheAlaPheA 1668 	Dp	6395 ACAIGCA
ò	668 rgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaileValLeuLeuSerileM 16	δλ	1935 alProVa ::
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දු දු	1728 lymetArgAlaLeuLeuHisThrValMetGinAlaLeuProGinValGiyAshLeuGiyb 1748 	qq	626
ò	748 euLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspL 17	à	01
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ολ	88 heGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleM 180	qu	0
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8	808 etLysAspProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrVall1eSerP 182	qq	::: 6866 GGGCCTA
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3 8	868 luAlaGluLeuGluLeuGluMetLvsThrLeuSerProGlnProHisSerProLeuGlvS 188	δ	2135 erGlyAe
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	353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 37	433 hrLysGlnArgGluSerGlnLeuMetArgGl 1202 CCAAGCAGCGGAAAGCCAGCTGATGCGGGAAGCCAGCTGATGCGGGAAAGCCAGCTGATGCGGCAGGGAAAGCCAGCTGATGCGGCAGGGAAAGCCAGCTGGCAGCAGCCCGGCAGGCA
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Glus 1819 ||||| GAGT 5455 AlaG 1839 ||||| GCCC 5515 Alas 1919 |||| GCCT 5755 Argv 1719 ||||| CGAG 5155 AsnL 1859 ||||| AACA 5575 Leus 1879 |||| |CTCA 5635 valA 1899 : cccG 5695 ---- 1927 LeuA 1679 ||||| CTGG 5035 AsnL 1699 |||| |AACG 5095 GlnA 1739 |||| CAGG 5215 AlaA 1759 |||| GCAG 5275 GlyL 1779 ||||| GGCC 5335 Vals 1799 |||| |GTCT 5395 ---- 1927 [|||| TCAG 4975 TGA 5815 3GCC 5875 --- 1927 TAG 5935 --- 1927 TAG 5995 --- 1927

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                                                        TCTGGGGTCAGCCGAACGCACTCTCTGCCCAATGACAGCTACATGTGTCGGC
                                                                                                                IleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP
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                                                                               ThralaGluargSerLeuGlyHisargGlyTrpGlyLeuProLysalaGlnS
                                                                                        ValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProL
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122 CONTOUNCEMENT CONTOUR CONT

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2136 luleuMapThrGluleuSerTrplleSerGlyAspleuLeuPPOSerSerSinGlude 6647 AgrTGGAACACGGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT	LeuProSerSerGlnGluG 2145 Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22	Qy 23 SerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgArgArgAla 4	A 2185 Qy 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 6 6826 G 6826 Db 441 CCGAGGACTCGGACACCCCGGAGCTTCATGCGGCTTCAACGACCTGTCGGGGCCGGGG 5	Qy 63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG 82	P 2225 P 2225 Qy 82 lyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP	2245 Qy 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV	2265 Qy 122 alileLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspileAlaCysA	Oy 142 spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlaV 1	Qy 162 alGlumetValValLysMetValAlaLeuGlyllePheGlyLysLysCysTyrLeuGlyA 1	rTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuA 20 	Qy 202 spleuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA 2 Avnd Morphogenesis by 921 AcctGcAGAACGTCAGCTCAGCTGTCAGCTGTCGTGTGCGACTCAGCTCAGGA GACCTGTGTGTGTGTGCGACCGCTCAGGG 9	Qy 222 laileAsnArgValProSerMetArgileLeuValThrLeuLeuLeuAspThrLeuProM 24	Qy 242 etLeuGlyAsnValLeuLeuLysPhePheValPhePheIlePheGlyIleValGlyV 262	Qy 262 alglnLeuTrpalaglyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP 282	82 roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI 3 	02 leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLe 	22 lyGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerA 3 :::	36 Gng Ailtheil Sylfa Carabay Cramary Britan Carabar Cramary C
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Score: Score: Best Local Similarity: 65.0% Conservative: 208 Best Local Similarity: 56.5% Mismatches: 536 Query Match: 10 Gaps: Caps: 64 US-09-611-257A-24 (1-2287) x US-10-483-467-3 (1-7898) Qy 188 CCGGGGGATGCCGGGGACGCGGCCAGCAGAGGTGCTGC-CGGCCG 243 Qy 23 SerAspProProGlyProArgLeuAlaArgCly	35 Th.A. garge- 295 GCGCCCCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Db 1065 ACCTTCCTGCGGCCGTACTACCAGACGGAGGAGGGCGAGGAGACCCGTTCATCTGCTCC 1124 Qy 305 GlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 324

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PRIOR APPLICATION NUMBER: US/09/398,522
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 3993
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CAGNAIG - a gene encoc FEATURE:
LOCATION: (373)...(3993)
US-10-930-301-51
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ON: CACNAIG POLYNUCLEOTIDE POLYPEPTIDE AND
ON: METHODS OF USE THEREFOR
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ION NUMBER: US/10/930,301
ATE: 2004-08-30
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US-10-930-301-51
; Sequence 51, Application; Publication No. US2005; GENERAL INFORMATION:
; APPLICANT: Issa, Jean; TITLE OF INVENTION: C; TITLE OF INVENTION: C; TITLE REFERENCE: JHU15; CURRENT APPLICATION N; CURRENT FILING DATE:
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Mismatches:
Indels:
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Score:
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Best Local Similarity:
Query Match:
DB:
; ORGANISM: Homo US-10-377-139-8
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US-10-377-139-8
; Sequence 8, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Use MacKinnon, Alice
; APPLICANT: Lee MacKinnon, Alice
; TITLE OF INVENTION: Voltage Sensor Domains Of
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; SOFTWARE: PALENTIN VERSION 3.1
; SEQ ID NO 8
; TYPE: DNA

TYPE: DNA
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                                     Length:
Matches:
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1476 1536 1044 1104 1224 1401 437 1281 867 924 357 397 417 477 497 567 984 --- caccaageaccccgcactaccatggaagactaag AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln ProArgGluAsnGlyMetArgSerCysArgSerValProThrheuArgGlyGluGlyGly SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu AspTyrGluThrTyrAsnSer - - - GÉCOGTGAGTÉCTGCCTÓTCCAAGGACGACGTCTACGÁCTTTGGGGCGGGGCGCCCAG MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer ArgAlaSerPro-GluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuPr oProProSerThrProThrPro-----SerGlyGlyProProArgGlyAlaGluSerVa oArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVa lHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluValAlaProSe 1HisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPr :::|||||||::: TCGGGCGACAATGGGATAATGGGCTGCCATGAGATCCCCCCCGCTCAAGGAGCAG HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHis-------- decccedadeccccecccccaaaccreaeccc----------HisHisHyrHisLeuGlyAsn-GlyGlyProProCysSerLeu-1045 585 625 925 378 398 1105 418 438 478 1342 498 1402 518 306 1438 548 567 605 g 8 8 6 8 6 6 6 6 음 상 음 6 B 6 ሪ ዌ ሪ 6 6 6 상 임 상 임 \$ B \$ Ω 8 셤 8

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US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. US20020150911A1
; Patent No. US20020150911A1
; APPLICANT: Dictrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT PILING DATE: 2001-08-23
; PRIOR PILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
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cacccggcTgCTCCATCCATGTGCACCAGCCACTACCTGGACATCTTCATCACC APheaspasnLeuGlyGlnalaLeuMetSerLeuPheValLeuAlaSerLysAspGly

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ò	2066 ValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIle 2085	Percer Best I	Percent Similarity: Best Local Similarity: Onerv Match:
ОЪ	5842 CTGTCGGTCTGGCTGAAACATGACA	DB:	
ò	2086 GlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla 2105	-60-SD	611-257A-24 (1-22
οp	5869	γo	12 ThrProPro
ò	2106 ProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeu 2125	qa	207 TCCCCGCCT
ф	5896 CCC 5913	, ÅÖ	26 ProGlyPro
ò	2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGlu 2145	qu	267 CCCGGACCCC
đ	5914	δ	46 ArgAspSerF
ò	2146 ProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrGlnSerCys 2163	qa	279AGC
qa	5950 CAGTGTCTGCCAGAAAGGCCCAGAAAAGGCCACTGGCACTGGAACCCTCCCCAAGA 6009	δ	66 AlaGlySerT
ò	2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerlleAlaValSerCys 2183	qa	327
qq	6010 TTGCGCTG-CAGGGCTCCTGGGCATCTCTGCGGTCACCAAGGGTCAACTGT 6059	ò	86 ProAlaLeuA
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qa	6060 ACCCTCCTCCGGCAGGCCACGGGAGCGACGTCGCTGGACGCCCAGCCCCAGCAG-CTC 6118	ò	106 CysLeuArg1
ò	2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSer 2219	qq	405 TGCATCAAG
qq	6119 CGCGGGCAGCCTGCAGACCACGCTCGAGGACAGCCTGAGCGACAGCCCCCGGCG 6178	٥٨	126 AsnCysValT
ò	2220 IleSerIleAspProProGluSerGlnGlySerArgProProCysSerProGly 2237	qu	465 AACTGCGTG
QQ	6179TGCCCTGGGGCCGCCCGCCCTGCTCCGGGACCCCGGGC 6217	ζÓ	146 CysArgileI
ò	2238 ValCysLeuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257	qq	525 TGCAAGATC
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δ	2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277	qa	585 CTCAAGATG
QQ	6278 GCGGGGGGCGCGCATCAGCGCAGCCAGCCAGCGGGGGCTCCACCAGCCCGGGCTG 6337	γ	186 ArgLeuAspE
RESULT US-09-	SULT 15 -09-935-541-3	qa	645 CGCCTGGAT
; Sequ	Sequence 3, Application US/09935541	ò	206 ValSerPhes
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	OF INVENTION: AND USES	qq	765 GTGCCCAGT
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PRI .	PRIOR APPLIANCE DATE: 09/404,650 PRIOR APPLIANCE DATE: 1994-09-20	qa	825 Greerecre
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Alignment Scores:

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Length:
Matches:
Conservative:
Mismatches:
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۶ و م	1739 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1758 	qq	5878 AC
'n	759 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 177	ò i	1 580
qq	4989 GCTCTCGGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGTGCGAGGGC 5048	a à	5908
λ i	79 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 179	. qa	103 AL 932 TC
gg ;	49 ATGAGCCGGCATGCCACCTTCGAGAACTTCGGCATGGCCTTCCTCACACTCTTCCAGGTC 510	δ	2125 Let
λ dd	1/99 SeringlyAspAsniipAsnGlylleMeCLySAspProserArgAspCysAspGin 1817	qa	5953
}	818 G]userThrCvsTvrAsnThrValIleSerProIleTvrDheValserDheVal 183	λσ	2145 Glı
à g		qa	986
<i>ك</i> ر	36 LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu 1	දු දු	2163 Cyr 6046 AG
qq	GCTCATCAACGTGGTGGTGGCTGTGATGAAGCACCTGGAC 52	ò	2183 Cy
oy B	1856 GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluLeuGluMet 1875 	ପ୍ର	on a
λΌ	876LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro 189	δ	O.
qq		තු ර	ស ៤
ΟŻ	1894	<i>∂</i> 7	
qq	Ø	<u>a</u> à	6215 GC
ò	19	දු දු	
ΩÞ	5466 TACTCGCCTGC-CCAGGAGAACCTGTGGCTGGACAGCGTCTCTTAATCATCAAGGACTC 5524	ò	257
ò	<pre>18 AlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProVal 1</pre>	g qa	31
Ωp	rgaccar	ò	277
λo	938 ProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 195	QO O	37
Dp	567 CATCTTCCACCACTACTCCTCGCCTGCCAGAAGTGTCA561		
<i>ኤ</i> 8	1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977 	Search Job tir	completed ne : 5447.0
ζ	978 GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 19		
QQ			
Qy	1998 AspThrSerCyslleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017		
qa	5705 TCTCGAGGACCCCACAGG 5722		
ò	leProLysLeuProPro		
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QΩ	5774 CATGCGTGTGGGAGACCTGGGCGAATGCTTCCTCCCCTTGT-CCTCTACGGCCGTCTCGC 5832		
ò 1	045 AlaileArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSer 2		
a :	835		
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                                                                      --GCAGTCAAGCACCCCCAAGTCCCT
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Command line parameters:
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-Q=/abss/ABSSWEB spool/US09611257/runat_10072006_064129_7044/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss08
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=7
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Sequence 31661, Application US/11266748A

Publication No. US20060134663A1

General Information:

APPLICANT: Harkin, Paul

APPLICANT: Mulliagn, Rarl

APPLICANT: Mulliagn, Rarl

TITE OF INVENTION: Transcriptome Microarray Technology and
TITE OF INVENTION: WHERE: US/11/266,748A

CURRENT FILING DATE: 2004-11-03

PRIOR PRIOR DATE: 2004-11-03

PRIOR PLING DATE: 2005-03-14

PRIOR PLING DATE: 2005-03-14
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 56474
LENGTH: 8079
TYPE: DNA
CRANISM: HOMO Sapiens
US-11-266-748A-56474
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j Sequence 56474, Application US/11266748A

j Publication No. US20060134663A1

j GENERAL INFORMATION:

j APPLICANT: Harkin, Paul

j APPLICANT: Mulligan, Rarl

j TITLE OF INVENTION: Transcriptome Microarray Technology and

j TITLE OF INVENTION: Methods of Using the Same

j TITLE OF INVENTION: Methods of Using the Same

j FILE REFERENCE: 55815-0102 (319189)

j CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2004-11-03

j PRIOR APPLICATION NUMBER: EP 04105483.4

j PRIOR FILING DATE: 2004-11-03

j PRIOR FILING DATE: 2004-11-03

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j PRIOR APPLICATION NUMBER: EP 04105507.0
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; Sequence 3, Application US/11350336
; Publication No. US20060135751A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHAN;
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/11/350,336
; CURRENT APPLICATION NUMBER: US/10/033,026
; PRIOR FILING DATE: 2001-12-28
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1999-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
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Db	2836 GGGGCCCCCGGAGCGCGAGCGCGCGGCCCA 2875	ځ	1393 U.S. AraThr.JenAra
ò	1133 gSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGluGlyGluGluSerGlnAspGl 1153	; E	٠ -
QQ	2876 -GGCCCCGAGGCGGCGGCGCGCGCGCGCGCCCGGAGGAGGCGGC	3 8	, ,
ò	1153 uGlu	ý E	1 1
qq	2935 GAGCCCCGACGCGCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCGGCGC 2994	a à	י ה
ò	1163 rProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLy 1180	s ස	7 ~
qq	2995 CAAGGCCGAGCGCGCGCGCGCGCGCGCCCCCCGAGCGGGGCCCCCC	ìà) (
ò	1180 sSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSe 1199	ें दे	
Dp	3055 GAGCGGGCCCGGCCA 3093	gr :	ๆ เ
ó	1199 rGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGl 1217	ờ	1465 pCysAlaGluAlaSer :
qq	TGTGGA	qq	m
λ	1217 yArgLeuAlaArgThrieuArgThrAspAspProGl 1229	λΌ :	48
qq	3154 GAAGGAGGCTGAGATAGTGGAAGGACGACGACGAGGAAGCTCCGGAACCACCAGCCCG 3213	අධ (m ·
ò	1229 nLeuAspGlyAspAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAl 1249	ò i	20
qq	3214 GGAGCCACACTGTGACCTGGAGACCAGTGGGACTGTGACTGTGGGTCCC 3262	ପୁ	m ·
ò	1249 aTrpValArgSerArgieuProAlaCysCysArgGluArg 1262	ý i	52
QQ	3263ATGCACACACTCCCAGCACCTGTCTCCAGAAGGTGGAGGAACAGCCAGAGGA 3315	Q	333
ò	1263AspSerTrp 1265	δ i	54
qq	::: 3316 TGCAGACAATCAGCGGAACGTCACTCGCATGGGCCAGTCAGCCCCAGACCCGAACACTAT 3375	a	g M
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qq	3376 TGTACATATCCCAGTGATGCTGACGGGCCCTCTTGGGGAAGCCACGGTCGTTCCCAGTGG 3435	an (ნ ' ი .
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ò	1314 sSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAl 1334	À ·	9
qq	 	d d	723
ò	1334 aGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuAr 1354	ठे र	φ (
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δ	1354 gSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLe 1373	දි ස්	ION IAShheuserheurich :
qq	3793 GGACTTGTGGAACATTCTGGACTTCATTGTGGTCGCGCCCTGGTGGCGCTTTGCTTT 3852	3 8	, ,
à	1373 uValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLe 1393	ර සි	1/1/ aAIGVaireunysreu :::::: 4876 GCGCTGATCAAGCTG
qq	3853 CTCGAGCTTCGTGGGAGGATCCAAAGGGAAAGACATCAATACCATCAAGTCTCTGAGAGT 3912	•)

4935 uAsnPheHisLysCysArgGlnHisGlnGluGluGluBlaAr -----AspThrArgAsn-----IleThrAsnLysSerAs GCTGGAGAGGGACTGCAGTCAGTATTTGGATTATGAGAAGGA rrieuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTy nCysLysProTyrTyrSerAspTyrSerArg-----PheArgLe ACCCCTGACACGGTACATGCCCCAAAACCGGCAGTCGTTCCAGTA uCysThrSerHisTyrLeuAspLeuPheileThrGlyValileGl nrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAl eMetGlylleThrLeuGluGlulleGlu-------Va rSerLeuLysProlleGlyAsnileValValIleCysCysAlaPh :rTyrArg----TrpValArgHisLysTyrAsnPheAspAsnLeuGl aValGlyValAspGlnGlnProlleMetAsnHisAsnProTrpMe CACCTTC-----CAGGAGCAGGGGACAAGGT sArgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGl gProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValVa GCCCCTCAAGACCATCAAACGCTGCCCAAGCTCAAGGCTGTGTT eSerPheLeuLeulleValAlaPhePheValLeuAsnMetPheVa

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Db 5962 GTCTGTCTCCTGGGGCACTCA Qy 2031 GlyArgSerProLeu-AlaGl	2070 rCysPro : 6202 cAGCCC 2090 gSerGly 6241 GCCCGT	2110 6300 2128 6360 2146	6417 CGGGGCTGC 2157 erValGluT 6477 AGCGGGGCC 2177 isSerIleA 6537 TC	Qy 2197 er	6768 2235 6828 6888 6948 6948
1737 tGlnalaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheilePh 1757		52LysHisLeuGluGlu-SerA 18	TGAGATGCTGAAACACATGTCCCCGCCTCTGGGGCTGGGGAAGAATG 545 ValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAla 191 ValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAla 191	ProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 195 CAAGCTGGCCCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGGAGTT 561 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGly 197 ::: GAGGAAGGAGATTTCCGTTGTGTGGGCCAATCTGCCCCAGAAGACTTTGGACTTGCT 567	1987 GlySerIleLeuSerVal
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yGluGlyGlyGlyBroProCysSerLeuAspTyrGluThrTyrAsnSerSerAs
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                                                                                APPLICANT: Lipscombe, Diane
APPLICANT: Lipscombe, Stephanie
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THER
FILE REFERENCE: B1055/7000
CURRENT APPLICATION NUMBER: US/11/350,336
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US/10/033,026
PRIOR FILING DATE: 2001-12-28
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 5, Application
; Publication No. US20066
; GENERAL INFORMATION:
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ORGANISM: Homo sapier;
FEATURE:
NAME/KEY: CDS
; LOCATION: 146..7162
US-11-350-336-5
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ACCTGCGGCCCGACATGAAGACGCACCTGGACCGGCCGCT 2595 2115 2175 :::|||||| | |||::: TTCTGGCCATCGCTGTGGACAACCTGGCCAACGCCCAAGA 2295 ---Phe-PheserProserValAspg 1022 uArgLysSerLeuLeu------1048 2715 rgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGl 1153 2235 1014 lySerArgArgThrSerSerSerGlySerAlaGluProGl 1088 930 890 ACGGCGCGCGGGGCCCGTGGGAGGCAAAGCCCGACCTGA GCGTCGACCTCCGCGCAGGCACCGCCACCGCGACAA AGCGGCCGCGCACCGCAGCCACAGGAGGAGGCCGC euValAlaljeLeuValGluGlyPheGlnAlaGluGlyAs er------ProHisSerProTrpSerAlaAlaSerSe ysasnPheaspSerLeuLeuTrpalaIleValThrValPh ||||||||||||| |ccaactTcGacaccTTcccTGccGccaTccTcAcTGTTT rpAlaAlaLeuTyrPhelleAlaLeuMetThrPheGlyAs ||||| |GCGAGGCGCTGTACAGCGAGATGGACCCCGAGGAGCGGCT aThrProMetSerHisProLysSerSerThrGlyVal GGGACCAGGACCGAGCAGAGGCCCCGAAGGCCGAGAGCGG erArgAsnSerLeuGlyArgAlaProSerLeuLysArgAr ::|||::: cgcggagcgagcgcggccgaggccca-----euValArgPheLeuProAlaLeuGlnArgGlnLeuValVa snValAlaThrPheCysMetLeuLeuMetLeuPhellePh AGATGGAAGAAGCAGCCAATCAGAAGCTTGCTCTGCAAAA luProAsp----

1433	09 1544 1G1yvalValValGluAsnPheHisLyse 4381 GGCTTTGATCATCATCATCTTC 1564 GArGArGGluGluLysArgLeuArgArg] 4423 GATGTCTGAATGCAGCG 09 1584 nMetAlaGluAlaGluCysLysProTyr' 4771 CGCCATCAGCGCCAAACCCTGACAGGG 09 1622 yLeuAsnValHisHisLeuCysThrSerHis' 4531 TAAGACGTGGACATTTGTGGTCTCCCCGG 09 1622 yLeuAsnValHisHisLeuCysThrSerHis' 4531 TAAGACGTGGACATTTGTGGTCTCCCCGG 09 1642 aLeuLysIleCysAsnTyrIlePheThr' 1642 aLeuLysIleCysAsnTyrIlePheThr' 1652 uValAlaPheAlaPheAcatCGTGTTCACACAC 09 1662 uValAlaPheAlaPheArgArgArgArgCTGAAGTTCACACAC 1662 uValAlaPheAlaPheArgArgTrCACACACACACACACACACACACACACACACACACACA
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| Control | Cont pThrargasn----IleThrasnLysSeras 1465 pValArgHisLysTyrAsnPheAspAsnLeuGl 1484 uAlaSerLysAspGlyTrpValAspIleMetTy 1504 STyrLeuAspLeuPheileThrGlyValileGl 1622 GCCCTTTGAATACTTCATCGCCCATGATAGC 4590 : | | | | GTTCTATGATGCACCCTATGAGTACGAGCTGAT 4650 eGlnAspArgTrpAsnGlnLeuAspLeuAlail 1682 |:::||| ||||||| CAGAGATGCTGGAATGTCTTTGACTTTGTCAC 4770 GTCCACGGGAGAAGGCTGGCCCATGGTGCTGAA 4260 1717 sCysArgGlnHisGlnGluGluGluAlaAr 1564 rTyrSerAspTyrSerArg-----PheArgLe 1602 aValGlyMetArgAlaLeuLeuHisThrValMe 1737 uGlyLeuLeuPheMetLeuLeuPhePhellePh 1757 ::||||||||:: yAspLeuGluCysAspGluThrHisProCysGl 1777 rValllePheValPheGluSerValPheLysLe ::: ||||||| AGTAACAGAGATTGCGGAAACGAACAATTTCAT rllelleArglleMetArgValLeuArglleAl :::|||:: ------TTCCTCCGCCTCTTTCGAGCTGC gLeuGluLysLysArgArgSerLysGluLysGl |||||||||| sccrGGAGAGAGGGGCTTGCATTGACTT pglnglnProlleMetAsnHisAsnProTrpMe uHisTyrGlnGlnProGlnIleLeuAspGluAl ::: |||||||||:::::::: rLeuGluGluIleGlu------Va :::||| ||||||||:::

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ΩÞ	5035 CAGCATCAACAACAACAACTTCCGGACGTTTTTGCAAGCCCTGATGCTGTTCAG 5094	a ;	/U TCAGATGCAGAGCATAACCCG
ζ	7 gValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCy ::: :::	<u> </u>	6130 CCAGGGTCGAGCGCCTCCATGCCC
qq	5095 GAGCGCCACGGGGGAGGCCTGGCACGAGATCATGCTGTCCTGCCTG	ò	2070 rCysProLeuThrArgSerSer
δ	1815 sAspGlnGluSerThrCysTyrAsnThrVallleSerProlleTyrPheValSe 1833	7 E	6190 CAGCCCATGAAGCGCTCCATCTCC
QQ	5155 TGATGAGCAGGCCAATGCCACCGAGTGAGTGACTTTGCCTACTTCTACTTCGTCTC 5214	1 8	0 0
ò	1833 rPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet 1851) E	
QΩ	5215 CTTCATCTTCCTGTGCTCCTTTTCTGATGTTGAACCTCTTTGTGGCTGTGATCATGGACAA 5274	}	110 22-2-2
δλ	1852LysHisLeuGluGlu-SerA 1858	ें र	IIO delectro de la ligha de la
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δγ	1858 snLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThr, 1878	à t	0 0
Ор	::	au .	B AGAAGGGGCCCAGC
ó	1878 eu-SerProGlnProHisSerProLeuGlySerProPheLeuTrpProglyValGluGly 1897	ò	
qq		QQ	6405 CGGGGCTGCCCCGGGAGAGGGGCCC
è	Val AsnSerThrAsnSerPro[vsProG]vAlaProHisThrThrAlaHisTleG]vAla 191	λō	2157 erValGluThrGlnSerCysArgAr
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3 8		λ	2177 isSerIleAlaValSerCysLeuAs
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qu	5608 GAGGAAGGAGATTTCCGTTGTGTGGGCCAATCTGCCCCAGAAGACTTTGGACTTGCT 5664	ò	2205GlyGlyProGlySerArgPr
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δλ	1997AlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGln 2014	ें र	
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			Jence 7. Application US/1135033

2223 2128 CCAACAGCTGGCCAGGAGCCGGGACCCCACCCACAGG 6635 2146 2197 6575 -----GinGlySerArgProProCyss, 2235 6228 6287 6347 2157 6464 2177 -SerLeuAspVa 2053 ysAspProProGlu-ThrArgSerSerLeuGluLeuA |||||||::: |TGCCACGCAGGACAGGAAGCAGAGGTCCCTGG GlyAspLeu-----LeuProSerSerGlnGluGluP 3GGGCCCTGATGGGGAGCCCCAGCCTGGGGCTGGAGAG ArgArgProGlyPheTrpLeuAspGluGlnArgArgH CCCTTGCTGTCAACATCTGGTGCTAGCACCCCCGGCC ------ValCysLeuArgArgAlaProA CTTTCCGAACACACGCCTGCTGCAGAAAACCCCC erPheTrpGlyGlySerSerIleGlnValGlnGlnAr || |-------------------ACGCTGGCCCAGCG erLysHisIleArgLeuProAlaProCysProGlyLe GCCGATATGGATGCCGCACCAAGCAGTGCTGTGGGGGC |||::::||| AGGCAGCCCTCATCCTCCTCGGAGAAGCAGCGCT AspSerGlySerGlnProArgLeuCysProSerProS -----SerLysAspProSerValSerSerProL rcrcaaattggcrcrdacccrtaccrgggggaggcgrc CACTICGCCGGGGCTCAGACCAGCCTCCTGCCTICT spLeuLeuSerGluValSerGlyProroleu-----Ser 2279

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APPLICANT: Lipscombe, Diane
APPLICANT: Schorge, Stephanie
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USE;
FILE REFERENCE: B1055/7000
CURRENT APPLICATION NUMBER: US/11/350,336
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US/10/033,026
PRIOR FILING DATE: 2001-12-28
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
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765
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Matches:
Conservative:
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; TYPE: DNA
; ORGANISM: Homo sapie:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..6856
US-11-350-336-7
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Best Local Similarity:
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1737 gvalserThrGlyAppAnTrphanGlyIlaketLyakep		; Sequence 9, Application US/11350336 ; Publication No. US2060135751A1 ; GENERAL INFORMATION: ; APPLICANT: Lipscombe, Diane ; APPLICANT: Schorge, Stephanie ; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF ; TILE REFERENCE: B1055/7000 ; CURRENT APPLICATION NUMBER: US/11/350,336 ; CURRENT FILING DATE: 2006-02-07 ; PRIOR FILING DATE: 2001-12-28 ; PRIOR FILING DATE: 1999-03-12 ; PRIOR FILING DATE: 1999-03-13 ; PRIOR FILING DATE: 1998-03-13 ; NUMBER OF SEQ ID NOS: 28
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	CEI: CDS	δ	286
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Alignment scores Pred. No.:	3.25e-72 Length:	ò	306
Score: Percent S	1693.00 Matches: 37.1% Conservative:	qa	. 062
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                                                        aGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValAs
                                                                                               ----cccaacacacada
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1277 GAAATGACCT	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT 762
8 6 8 6 8 6 8 6 8 6 8	6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

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4167 GTTTCGG 1539 ILEUASH 1539 ILEUASH 4227 TGTCAAC 1559 UGLUGLU 1579 GCAGGGG 1579 GSETLYS 4317 GGCTTGC	Oy 1599 gPheArgLeuLeuval 1617	Oy 1697 lAsnLeuSerLeuProlleAsn	Qy 1777 uGlyLeuGlyArgHisAlaThr bb 4890 CAGCATCAACCGACACAACAAC Qy 1797 gValSerThrGlyAspAsnTrp bb 4950 GAGTGCCACTGGGGAGGCCTGG Qy 1815 sAspGlnGluSer Db 5010 CGACCCACTGCCAACGCCAGG Qy 1832 lSerPheValLeuThrAlaGln Db 5067 CTCCTTCATCTCCTCTGTTCC Qy 1852 sHisLeuGluGluSerAsnLys 1852 sHisLeuGluGluSerAsnLys ::: Db 5127 CAATTTCGAATACCTCACGCGC Qy 1864 uAlaGluLeuGluAlaGluLeu cy 1864 uAlaGluLeuGluAlaGluLagluLeu
1198 aSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyAr 1218	254 gLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIl 126	AGGAGTCTTCACCTTTGAGATGGTCATAAAGATGATAGACTTGGGCCTGCTGCTGCACCC 362 uGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVa 136	3807 ACTCAAGGCTGTGTTTGACTGTGGTGAACTCTCTGAAGAATGTCTTGAACATCTGAT 3866 1428 IlleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLy 1448 ::::
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CITCTATGTGGTCTACTTTGTGGTCTTCCCTTTTTTCTT 4226 inProThrilelleArgIleMetArgValLeuArgIleAl 1717 /sMetAlaValGlyMetArgAlaLeuLeuHisThrValMe 1737 euPheGlyAspLeuGluCysAspGluThrHisProCysGl 1777:::||||||::::::|
rttttGGAAACATTGCCCTTGATGATGGC-----AC 4889 11PheArgAsnPheGlyMetAlaPheLeuThrLeuPheAr 1797 :gGjuGluLysArgLeuArgArgLeuGluLysLysArgAr aGluAlaGlnCysLysProTyrTyrSerAspTyrSerAr JIIII JATGGACATITGTGGTCTCTCCACCCTTTGAGTACTTCAT euleuserijeMetGlyijeThrLeuGludjujjeGluVa srThrCysTyrAsnThrVallleSerProlleTyrPheVa ----TGCAGTCTGGAAAAGAATGAGAG snvalvalthrMetAlaMetGluHisTyrGlnGlnProGl InPhevalLeuValAsnValValIleAlaValLeuMetLy pasnGlyjjemetLysasp-----ProSerargaspCy scgaardc - - - eggagcgactrtecctartrtrarriter ------GluGl lValValGluAsnPheHisLysCysArgGlnHisGlnGl al His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phell GATCATCACCTTC-----rsGluAlaLys------

euGlu--:: Page 24

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2077 SerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLys 2096	110 AACCTAAG	1	CTTCTGG laSerPr :::: CTGCCCA	ESULT 7 S-11-313-450-9 Sequence 9, Application US/11313450 Sequence 9, Application US/11313450 Publication No. US20060110778A1 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Ehring, George R. TITLE OF INVENTION: High-Throughput Screens For Identifying TITLE OF INVENTION: Selective Persistent Sodium Channels Channel Blockers FILE REFERENCE: 17407 CIP (AP) CURRENT APPLICATION NUMBER: US/11/313,450 CURRENT APPLICATION NUMBER: 09/989797 PRIOR FILING DATE: 2001-11-20 PRIOR FILING DATE: 2000-11-22
AGCTGCGTGTGGGCGCATCAGTTACAATGACAT oglnProHisSerProLeuglySerProPheLe	1918 1918 5533 5593	AACAGAACAAAACCACCAGAGATCAGACTCCTGGAGGCCTGTCCCAGATGG 5653 OGluGluValProValProLeuGlyProAspLeuLeuTh 1945 OGluGluValProValProLeu	5893 1977 5953 1990 6013 2010	
5187 C 1873 - 1891 u 5294 A 5354 A	1906 1907 1907 1919 1924 1924	5594 1932 1945 5714 5774 1955	Db 5834 AGGACGTACTTTATGAGGCCAGAGG Qy 1968 rThrAlaGluArgSerLeuGlyHis Db 5894 TGGGCAGCCAGGAGCACTGGCTG Qy 1978 -GlyTrpGlyLeuPro Db 5954 CGGATGGGAGCCCAGCCTGGCC Qy 1990 euSerValHisSerGlnProAlaAs Qy 1990 euSerValHisSerGlnProAlaAs Db 6014 TGGCGCAGAAACACAGCCGGCCC	2010 i 6068 C 2029 r 6128 C 2037 l 6188 A

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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for W
; SEQ ID NO 9
; LENGTH: 6051
; TYPE: DNA
; ORGANISM: Homo sapiens
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QQ	ACAGCGCTCAACGGCACCAACGGCTCCGTGG 88
ολ	280SerLeuProLeuSerValAspLeuGluProTyrTyrG 292
Db	884 AGGCCGACGGCTTGGTCTGGGAATCCCTGGACCTTTACCTCAGTGATCCAGAAAATTACC 943
٥٨	292 lnThrGluAsnGluAspGluSerProPhelleCysSerGlnProArgGluAsnGlyMetA 312
qa	944 TGCTCAAGAACGGCACCTCTGATGTGTTACTGTGTGGG
δ	312 rgSerCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyGlyProProCysSerL 332
Db	981
٥٨	332 euAspTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrT 352
qq	982CCGGAGGCTCTGACGCTGGGACATGTCCGGAGGGCT 1015
ò	352 yrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnI 372
QQ	1016 ACCGGTGCCTAAAGGCAGGCGAGAACCCCCGACCACGGCTACACCCAGGTTCCT 1072
δλ	372 leGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleM 392
ОЪ	1073 TTGCCTGGGCCTTTCTTGCACTCTTCCGCCTGATGACGCAGGACTGCTGGGAGCGCCTCT 1132
ò	392 etTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuLeulleI 412
qa	1133 ATCAGCAGACCCTCAGGTCCGCAGGGAAGATCTACATGATCTTCATGATCTTCATGTCATGT 1192
δ	412 leValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerG 432
ΟD	1193 TCCTGGGGTCCTTCTACCTGGTGACCTGATCCTGGCCGTGGTCGCAATGGCCTATGAGG 1252
ογ	432 luThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnA 452
Db	1253 AGCAAAACC 1261
δ	452 laSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrL 472
QQ	1262 AAGCCACCATCGCTGAGACCGAGGAAAGGAAAAGCGCTTCCAGGAG1308
δ,	472 euValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyV 492
qq	1309GCCATGGAAATGCTCAAGAAAGAACACGAGGCCCTCACA 1348
٥٧	492 alArgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerG 512
qq	:: :: :: :
٥٨	512 lySerCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 532
QQ	1400 CCCCAGTAAACAGCCATGAGAAGAAGAAGC
ολ	532 isHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValP 547
qq	1429AAGAGGAGAAAAACGGATGTCTTCAGGAACTGAGGAGTGTGGGGAGGACAGGTCTCC 1483
ò	547 roArgAlaSerProGluIleGlnAspArgAspAlaAsnGlyS 561
Ωp	1484 CCAAGTCTGACTCAGAAGATGGTCCCAGAGCAATGAATCATCTCAGCCTCACCGTGGCC 1543
ò	561 erArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgG 581
рр	1544 TCAGCAGGACTTCTATGAAGCCACGTTCCAGC
ò	581 lyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysG 601
Ωp	1580 GGAGCATTTTCACCTTTCGCAGGCGAGACCTGGGTTCTGAAGCAGA-TTTTGCA 1632

CTGAAGGCTGTGTCCGGCGCTGTCCCTGCTGTGCGGT 3542	gGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuCy 1280 ::: gGaCaCCCACGCCCCAGGGAAGGTCTGGTGGCGGTTGCGCAAGACCTG 3593	sHisArgllelleThrHisLysMetPheAspHisValValLeuValllellePheLeuAs 1300 ::: :::	nCyslleThrlleAlaMetGluArgProLyslleAspProHisSerAlaGluArgllePh 1320 ::::	eLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysVa 1340 :::::: :::	IvalalaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLe 1360 	uAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSe 1380 	rGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgPr 1399 	OLEUArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSe 1419 ::: ::::::::: ::: TCTGAGAGCTCTGTCACGATTTGAGGGCATGAGGGTGGTGGTCAATGCCCTGGTGGGGGC 3989	rLeuLysProlleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIl 1439 ::::	eLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGl 1455 :::	uaspThrargasnIleThrAsnLysSerAspCysAlaGluAlaSerTyrAr 1472 :	gTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMe 1488 :::	tSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAs 1508	palavalGlyvalAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPh 1528 -::	elleSerPheLeuLeulleValAlaPhePheValLeuAsnMetPheValGlyValValVa 1548 	GluasnPheHisLysCysArgGlnHisGlnGluGluGluGluAlaArgArgArgGl 1567 : 	uGluLysArgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGl 1587 ::: ::: CAGAAGAAGTACTACAATGCCATGAAGAAGCTGGGCTCCAAGAAGCCCCAG 4521	ualaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLe 1607 AGCCCCATCCCACGGCCCCTGAAGTACCAGGGCTTCATATTCGACAT 4571
CTTCACTGAAGGC	gGluArgAs; ::: sgaCACCAC	sHisargil ::: craccacat	nCyslleTh : CAGTGGAGO	eleuThrle GCTTGAGTA	lvalAlaLe GGTGGCC	JASPGIYLE GACTTCCT	rG1yTh : ccresscrr	oLeuArgVa rcrGAGAGC	rLeuLysPr :::: CATCCCGTC	eLeuGlyVa ::: CATGGGCGT	uAspThrAr : CTTGCCTTT	g	tSerLeuPh :::: GGCCTTCT	palavalg1 ::: crccaggg	elleSerPh ::: GTCATTTT	GluAsnPh :::: TGACAACTT	uGluLysAr ::: :: GCAGAAGAA	uAlaGlnCy
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eValLeuThrAlaGlnPheValLeuValAsnValVallleAlaValLeuMetLysHisLe uGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeu-G CAGCGTGGCCACGGAGGAGGAGCACCGAGGCCCTGAGT---GAGGACGACTTCGATATGTT 1874 luMetLysThr ----- LeuSerProGlnProHisSerProLeuGly ----- SerP roPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaP GTCTGACTTTGCCG---ATGCCCTGTCTGAGCCACTCCGTATCGCCAAGCCCAACAGAT 1766 yAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheAr TTATGTCAAGTGGGAG------GCTGGCATCGACGACATGTTCAACTTCCA pCysAspGlnGluSerThrCysTyrAsnThrVallleSerProlleTyrPheValSerPh roHisThrThrAlaHis-----GlyP heserteuGluHisProThrMetValProHisProGluGluValProValProLeuGly-aPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSe rijeMetglylleThrieuGluGluIjeGluValAsnLeuSerLeuProlleAsnProTh rileileargilemetargvalLeuargilealaargvalLeuLysLeuLeuLysMetal 5145 CCTCCTCAGCCCCATCCTCAACACTGGGCCGCCCTACTGCGACCCCACTCTGCCCAACAG uCysThrSerHisTyrLeuAspLeuPhelleThrGlyVallleGlyLeuAsnValValTh sasnTyrIlePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAl gAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGl ylleMetLys----5040 1726 1786 $\boldsymbol{\omega}$

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323 ATGAGCACCTCTGCACCCCACCT----GTAGGATCTCTCCCAAAGAAACGTCAG
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AACTCCATTATAAAAAGCCATGGTTCCCCTCCTTCACATAGCTATTTGTATTTGTATTTGTA
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GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Rarl
TITLE OF INVENTION: Methods of Using the FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR PELICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PARENTIN VERSION 3.3
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1815-0102 (319189)
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APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A; CURRENT APPLICATION NUMBER: EP 04105479.2 PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR APPLICATION NUMBER: EP 04105482.6 PRIOR FILING DATE: 2004-11-03 PRIOR FILING DATE: 2005-03-14 PRIOR PRIOR FILING DATE: 2005-03-14 PRIOR PRIOR FILING 
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173 ySerLeuGluArgGluAlaLysSerSerPheAspLeuP 1725 GGAGTTGAACATGAAGGAAAAATTGCC	COASPTHrLeuGlnValProG1 1193 ::: ::: 1uHisGlnAspCysAsnGlyLy 1213 Coy spAspProGlnLeuAspGlyAs 1233 Coy rglleGlnAlaTrpValArgSe 1253 crallaTyrllePheProProG1 1273 crallaTyrllePheProProG1 1273 crallaTyrllePheProProG1 1273 cy sy crallaTyrllePheAspHisValVa 1293 cy sy crallaTyrllePheAspHisValVa 1293 cy crallaTyrllePheAspHisValVa 1293 cy sisLysMetPheAspHisValVa 1293	5521 5523 553 5613 661 661 6621 6621
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	1521 nProTrpMetLeuLeuTyrPhelleSerPheLeuLeulleValAlaPhe	hePheValLeuAs 1541
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> 0	1561 uGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysP. ::: 3661 AGAGTATAAGAACTGTGAG	ysArgArgSerLy 1581 ATCAGCGTCAGTG 3702
_	581 sGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyṛSe	ArgPheAr 1
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Qy 1835 LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	4639 AATATGGTCAGAATATGACCCTGAGGCAAAGGGAAGGATAAAACACCTTGATGTGGTCAC 1877 rLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro	Qy 1894	Db 4819 TGCAACC	Qy 1925HisProThrMetValProHisProGluGluValProValProLeuGlyPr 1941	oaspleuleuThrValargLys194 ::: GaTGAGGTAACCGTGGGAAGTTCTATGCCACTTTCCTGATACAGGACTACTTTAGGAA 503	 NAACGGAAAGAACAAGGACTGGTGGGAAAGTACCCTGCGAAGAACA	Qy 1949 SerGlyValSerArgThrHisSerLeu	Qy 1958ProAsnAspSerTy 1962 	1962 rMetCysArgAsnGly	1968SerThralaGluArgSerLeuGlyHisArgGlyTrpGlyLe 198 :::	Qy 1981 uProLysAlaGln	Qy 1992 lHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLe 2012 ::: 	Qy 2012 uLeuGln	Qy 2024 eProLysLeuProProProGly

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; ORGANISM: Homo sapiens
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an (16ACIGAGGAAITCAAAAA1GIACITIGCIAITIGGAATCITIG 23	ζ	116
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o d	CAGCTGAAATGGTATTAAAACTGATTGCCATGGGATCCATATGAGTATTTCCAAAGTAGGCT 23	ò	1185
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45 jyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluAspArgAlaSerProA 1165 hraspaspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeuSerLysGlyG 1245 1012 euValAlaLeuGlyGluHisAlaGluLeuArgLySSerLeuLeuProProLeuIleIleH 1052 52 isThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaL 1072 AAGCA------TTTTCCAAAAAGCCAAAGATTTCCAGGAGATAAGACAAGCAG 3049 55 laGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspL 1185 euProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaS 1205 :: ::|||||:::
ATGAGCCAGAGGCCTGTTTCACAGATGGTTGTTACGGAGGTTCTCATGCTGCCAAGTTA 3472 rg---AspSerTrpSerAlaTyrilePheProProGlnSerArgPheArgLeuLeuCysH 1281 73 ACATAGAGTCAGGGAAAGGAAAATCTGG------TGGAACATCAGGAAAACCTGCT 3523 rpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuL :::::::|||||||| rGTGCCTTATTGTTACATGGTCATGGTCATTGGAAACCTGGTGGTCCTAAACCTAT 39 laAlaHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpS CAGTTGATAACCCTTTGCCTGGAGAAGGAGAAGAAGCAGAGGCTGAACCTATGAATTCCG 72 euGlySerArgArg-----ThrSerSerSerGlySerAlaGluProGlyA ------ProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerG erGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgT |||||| | TCCCA---CGGTGGCACATGAACGACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGC 06 TTCACAATCCCAGCCTCACAGTGACAGTGCCA-------ATTGCACCTG ::: |----AGCAAAGTGAGATTAAAACCGGTCAAGCTCCT euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMet ---AlaSerThrSerSerT euValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerG ::|||:::|||:::||||::
TTCTGGCCTTATTATTGGCTCATTTAGTTCAGAC---AATCTTACAGCAATTGAAGAAG 12 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaL luArgIleGlnAlaTrpValArgSer-----ArgLeuProAlaCysCysArgGluA euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL erAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAla----:: | | | | ::::: CGGATAGTGAATAC----53 38 72 5 55 12 2 9 88 96 2 92 52 75 33 32 60 35 47 2

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  -GAGAGTGGGGAGATGGATT
                                                    --GGACTTGGACCCCTACTATGCAGACAAAAGACTTTCATAGTATTGAACAA
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                                 erValHisSerGlnProAlaAspThr-SerCysIleLeuGlnLeuProLysAspValHis
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Matches:
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                                                                                                                                                                          ; Sequence 8, Application US/11251465; Sequence 8, Application US/11251465; Publication No. US20060094061A1; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald; APPLICANT: Tomme, Peter; APPLICANT: Klaassen, Hubertus; TITLE OF INVENTION: Molecular Targets And Com; TITLE OF INVENTION: Inflammatory Diseases; TITLE OF INVENTION: Inflammatory Diseases; FILE REFERENCE: P30,172-A USA; CURRENT APPLICATION NUMBER: US/11/251,465; CURRENT APPLICATION NUMBER: 60/619,384; PRIOR FILING DATE: 2005-10-14; PRIOR FILING DATE: 2004-10-15; NUMBER OF SEQ ID NOS: 880; SEQ ID NO 8; SEQ ID NO 9; 
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43.3%
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 5507 AGCGTGTTTTGGGT
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ORGANISM: Homo sapiens
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Percent Similarity:
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2318 TGACTGAGGAATTCAAAAATGTACTTGCTATAGGAAATTTGGTCTTTACTGGAATCTTTG 2377 820 laLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProT 840	0 heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAs	933 euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953	972 rpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuL 992 1843 TGTGCCTTATTGTTTACATGGTCATGGTCATTGGAAACCTGGTGGTCCTAAACCTAT 2902 992 euValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerG 1012 1012 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaL 1032 1012 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaL 1032 1014 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaL 1032 1015 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaL 1032 1016 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaL 1032 1017 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaL 1032	032 euValAlaLeuGlyGluHisAlaGluLeuArgLySSerLeuLeuProProLeuIleIleH 105::::::::::::::::::::::::::::::::::::	TAAGAAGGAAACTATTTTTTAACCATACATACTTGCT .uMetLysCysProProSerAlaArgSerSerProHis ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::: :::: :::: :::: :::: :::: :::: :::: :::::
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1510 alGlyValAspGlnGlnPrOlleMetAsnHisAsnPrOTrpWetLeuLeuTyrPhelleS 1530 4271 TTAATGTAGCAGGCGAAATATGAATATGCCTCTCATCHGTATATTATTTTTTGCG 4330 1530 erPheleuLeuleulleValAlaPhePheValLeuLenBmberPheValGlyValValValGluA 1550 1550 sPPheHistyGCYSArgClnHisGlnGluGluAlaargArgArgGluGlu 1550 4331 TCTTTATCATCTTTGGGTCATTCTTCACTTGAATTGGTGCATCATAGATA 4390 1550 sPAMPHHistyGCYSARGCATTCTTCACTTGAACTTGTTGATGGTGCATCATAGATA 4390 1550 sPAMPHHistyGCAATCTTCACTTGAGCTTATGGTGTCATCATAGATA 4390 1560 pysArgleubrgArgLeuGluLySLySArgArgSerLysGluGluAlaargArgArgGluGluL 1569 1551 aAAATACTATAATGAACAGAAAAAAAAACAGAACAAAACAAAAACAAAAACAAAAACAAAAAA	
6	6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 7 B 7 B
1165 39G1/SerkspHisArgHisArgG1/SerLeuGluArgG1uAlaLysSerSerPheAspL 1185 3144 CGGATAGTGAATAC.	0y 1381 lyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuA 1401 Db 3851 GCTACTCAGATCTTGGCCCCATTAAACCCTTGGACACTTAAGACCTTAA 3910 Oy 1401 rgValleSerArgAlaGlnGlyLeuLysLeuLysLeuArgCaCACTGAGAGCTTTAAGACCCTTAA 3910 Oy 1421 ysProlleGlyAsnileValValileCysCysAlaPhebheileIlePheGlyIleLeuG 1411 Db 3911 CTTCCATCATGAATGAAGGAATGAGGGTCGTTGTGAATGCACTCATAGGAGCAATTC 3970 Oy 1421 ysProlleGlyAsnileValValileCysCysAlaPhebheileIlePheGlyIleLeuG 1411 Db 3971 CTTCCATCATGAATGACTATTGTGTCTTATATTCTGCTCATAGGAGCAATTC 3970 Oy 1441 lyValGlnLeuPheLysGlyLysPhePheValCys

us-09-611-257a-24.rnpbn

Pred. No.: 2.19e-69 Length: 6371 Score: 1633.00 Matches: 546 Percent Similarity: 43.3\$ Conservative: 376 Best Local Similarity: 25.7\$ Mismatches: 773 Query Match: 13.6\$ Indels: 434 DB: 8 Gaps: 74	Qy 35 ThrargargargMetGluArgalaProArgSerArgAsp 4	48	Db 210 AGCTGGCAAACAACTGCCCTTCATCTATGGGGACATTCCTCCCGGCATGGTGTCTAGAGCC 26 Qy 59 ProglyProglyAlaAlaGlyAlaGlySerThrGlutysAspProGlySerAlaAspSer 78	 270 CCTGGAGGACTTGGACCCCTACTATGC	79 GluAlaGluGlyLeuProTyrProAlaLe	TGCCACACCIGCTTIAIAIAIGCTITCICC sLeuArgThrValCysAsnProTrpPheGluArgVa	381 TTTCAGTCCTCTAAGAAGAATATCTATTAAGATTTTTAGTACACTCCTTATTCAGCATGCT 4	Qy 118 SerMetLeuValileLeuLeuAsnCysValThrLeuGlyMetPheArgPro 13 	AlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspP	Db 501 GACCAAAATGTCGAGTA 5	155 ellePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyIle ::: :::::	DD 519 CACITITACIGGAATAIATACITITGAATCACITGTAAAAATCACITGCAAGAGGCTICIG 3 Qy 174 -PheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValil 1		a)	rcagcrc	Oy 213 rValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuVa 2	233]Tht.en.en.en.Trianscrittenmectaritecters.coc.coc.coc.coc.coc.coc.coc.coc.coc.co		253 Dhephellephed vl]eValGluCeuTroAlaGluLeuTroAlaGluLeuLeuArdSsnArdCV	813 TCTGAGTGTTTGCACTAATTGGACTACAGCTGTTCATGGAACCTGAAGCATAATG	273 sPheLeuProGluAsnPheSerLeuProLeuSerVal		Qy 286AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCy 3	AAGGATCCAAAGATGCTCTCTT	Qy 303 sSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGl 3
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 Alignment Scores:

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	1749 598 1791 617 1851 637 1862
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TGTGCCTTATTG' euValAlaIleL' ::: ::: TTCTGGCCTTAT' luProAspPheP] :: ACCTGAT euValAlaLeuG' :: TGACTAGAATTA	AAGCA euGlySerGlyS aAGATCTGAATA laAlaHiSHiSG laAlaHiSHSGATT erAlaAlaSerS GTGGTTTTGGAA TTCACAATCCCA TTCACAATCCCA TTCACAATCCCA		hraspaspProG
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52,	3]vLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerG 138
	::: TCTTG 385
1381	LysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuA ::::: rcagalctrGGCCCCATTAAATCCCTTCGGACACTGAGAGCTTTAA
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1441	alGlnLeuPheLysGlyLysPhePheValCysGlnGlyGlu 14
1456	nIleThrAsnLysSerAspCysAlaGluAlaS 147
4091	cngcaagtccaadiccaaaiccaaaicituttgcccttatgaatgttagt
L 1	TyrargTrpValargHisLysTyrasnE GTGCGarGGaaaaaCCTGAAGTGAACT
4	uPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaV 151
4211	::: ::: SAAGTIGCAACTITIAAGGGAIGGACGAITATIAIGIAIGCAGCAGIGGAIICIG 42
1510	GlyValAspGlnC
4271	AATGTAGACAAGCCCCAAATATGAATATAGCCTCTACATGTATATTATTTGT
1530	nMetPheValGlyValValValGluA 1550 ::: ::
4331	TTATCATCTTTGGGTCATTCTTCACTTGAACTTGTTCATTGGTGTCATCATAGATA 439º
1550	sArgGlnHisGlnGluGluGluGluAla :::::: 3AAAAAGCTTGGAGGTCAAGACATCTT
	gArgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAl
4451	 aatgcaatgaaaagctggggtccaagaagcc
1589	nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCy
4498	AAGCCAATTCCTCGACCAGGGAACAAATCCAAGGATGTATATTTGACCTAGTG
09	SerHisTyrLeuAspLeuPhelleThrGl
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, ,	GGTAGAAAAGGAGGGTCAAAGTCAACATATGACTGAAGTTTTATATTGGATAAATGTGG 467
	PheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAla
4673	ATGTGTGC
1669	nePheGlnAspArgTrpAsnGlnLeuAspLe
4730	TACTTCACTGTAGGATGGAATATTTTGATTTTGTGGTTGTGATTATCTCCATTGTA

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Sequence 98, Application US/11263326
Sequence 98, Application US/11263326
GENERAL INFORMATION:
APPLICANT: Wullace, Robyn H
APPLICANT: Wullay, John C
APPLICANT: Wullay, John C
APPLICANT: Berkovic, Samuel F
TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
FILE REFERENCE: 1386/13/3
CURRENT APPLICATION NUMBER: US/11/263,326
CURRENT FILING DATE: 2005-10-31
PRIOR APPLICATION NUMBER: US 10/482,834
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PRIOR FILING DATE: 2004-10-86
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 98
LENGTH: 7008
TYPE: DNA
ORGANISM: Homo sapiens
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4684 CGCCCCTGAACAAACCAAGGAATTCTGACTTTGCACTCACCAACCA	Š	SerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAsp 161	δλ	935 ValProVal
1615 LeuPhelleThrGlyVallleGlyLeuAsnValValThrMetAlaNetGluHisTyrGln	අ	CGCCCCTTGAACAAAATCCAAGGAATCGTCTTTGATTTTGTCACTCAGCAAGCCTTTGAC 475	q O	657 ATTGAGCTC
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1655 ValPheGluSerValPheLysteuValAlaPheArgArgPhePheGlnAsp 1673 1674 ArgTrpAsnGTGGCTGAAATGTTTGCGTTGACGCACTACTTCACCTTT 4927 Qy 2015 1674 ArgTrpAsnGTInLeuAspLeuAlaIlevalLeuLeuSerIleMetGlylleThrLeuGlu 1693 Db 5828 1674 ArgTrpAsnGTInLeuAspLeuAlaIlevalLeuLeuSerIleMetGlylleThrLeuGlu 1693 Db 5828 1694 GLUILGGLAVAIAGCTTCGGGTAGTCATCCTGCATTGGGAATGTTCCTGGCA 4987 Qy 2035 1694 GLUILGGLUVAlAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgVal 1713 Db 5834 Db 5834 Db 5834 Db 5834 Db 5842 GCCGGAATTGGAGAATTCTTCCCAACCCTATTCCGAGTTGCTGCTTGTACTGTACCTGGTTGTAGAATACTTTGTTTCCCAACCCTATTCGAGTTGTAGTGTATTGAGAATACTTTGTTTCCCAACCCTATTCGAGTTGTAGTGTATTGGGAATTGTAGAATACTTTGTTTCCCAACCTATTCGAGTTCGTTGTAGTGTATTGGGGATTGTAGTGGTTTGATGAGGGATTGTGAGGATTGGGGATTGTAGTGTTGAAAGGGGTTTCGTACTGTACCTGGTCT 5101 Db 5861	qq	CAAAGCAAGCAGATGGAGAACATCCTCTACTGGATTAACCTGGTGTTTGTT	λo	995
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1774 HisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeu 1793	q	ATGTTCATCTTCCATTTTTGGATGTCCAATTTTGCATATGTGAAGCACGAG 521	ò	4 pAlaLy
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Qy 2134 eSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuLysLy 2154 Db 6053 CAGCGGGCAGAGGAAGGAAGGAAGGAAAGAGCCAAAAGAG 6100 Qy 2154 sCysTyrSerValGluThrGlnSerCysArgArgArgArgProGlyPhe 2169 Cy 1	APPLICANT: Wallace, Robyn H APPLICANT: Wallace, John C APPLICANT: Wallace, Samuel F TITLE OF INVENTION: NEW EPILEPSY MUTATIONS FILE REFERENCE: 1386/13/3 CURRENT APPLICATION NUMBER: US/11/263,326 CURRENT FILING DATE: 2005-10-31 PRIOR APPLICATION NUMBER: US 10/482,834 PRIOR FILING DATE: 2004-10-12 PRIOR APPLICATION NUMBER: PCT/AU2004/001051	; PRIOR FILING DATE: 2004-08-06 ; PRIOR APPLICATION NUMBER: US 10/451,126 ; PRIOR FILING DATE: 2003-10-08 ; NUMBER OF SEQ ID NOS: 179 ; SOFTWARE: Patentin version 3.3 ; SEQ ID NO 104 ; LENGTH: 7008 ; TYPE: DNA ; ORGANISM: Homo sapiens US-11-263-326-104	Alignment Scores:	Qy 1 MetLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg 20	76 CGGGCCGCGCTTAGGGCCGCCGCTCCTCGCC 59 ProGly	GAGGCGCATTGCTGAGAGCAGCTCAAGAACCACCAAAGGCCGATGGCAGTCATCGGGA 3 O

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316 ATTATAAAAGCCATGGTTCCCCTCCTTCACATAGCCC	a	2074 rArgSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGl 2094 ::: :::::::::	<i>∂</i> 6
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196 GGGAACCACTCAAGCGGCAAATCTGGAGGCTTTGATG 216 ValLeuArgProLeuArgAlalleAsnArgValProS	යි ර <u>ි</u>	2035 LeuAlaGInArgProLeuArgArgGInAlaAlaIleArgThrAspSerLeuAspValGln 2054 ::: 5834 ATCACAACCACTGCGTCGCAAGCAG	oy G
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82 TIGCTACATCCTAATGCTTATGTTAGGAATGGATGGA 193 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnA	යි රි 	1995 GlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGln 2014	Oy Dp
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157 PheAlaPhePheAlaValGluMetValV 	<i>ਨ</i> 업	5705 CACTGCTTGGACATCCTTTTTGCCTTCACCAGGGTCCTG 5746 1975 GlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSer 1994	අ _ධ
-09-611-257A-24 (1-2287) x US-10-473-173-94 (1-66	sn	1955 HisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeu 1974	ò
Score: Percent Similarity: 38.7% Conservative Best Local Similarity: 24.7% Mismatches: Query Match: 13.2% Indels: DB:	Scori Percy Best Quert	5597 AAGCTGĠĊAGACTTTGCAGATGCCŤŤĠĠĀĠĊĄŤĊĊſCTCCGĀĠŤĠĊĊĊAAGĊĀĀATACC 5656 1935 ValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr 1954 ::: ::: :::	da da
13-173-9	SU .	5567	ପ୍ର (
LENGTH: 6600 TYPE: DNA ORGANISM: Homo sapiens		AsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGly 19	δ
PRIOR FILING DAIE: 2001-03-29 NUMBER OF SEQ ID NOS: 498 SOFTWARE: PatentIn version 3.2		1879 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyVal 1898 ::: 5549 5566	Q G
; FILE REFERENCE: 38343-1/0034; CURRENT APPLICATION NUMBER: US/10/473,173; CURRENT FILING DATE: 2003-09-29; PRIOR APPLICATION NUMBER: US 60/279,411		1862 LysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeu 1878 ::: 5507 GCAGACCCTCTGAGGATGACTTTGAGACCTTCTATGAG	S S
APPLICANT: VAN ANDEL INSTITUTE TITLE OF INVENTION: Microarray Gene Expression P. TITLE OF INVENTION: Carcinoma: Prognosis and Drive Design Carcinoma		1842 LeuvalasnvalvalIlealavalLeuMetLysHisLeuGluGluSerAsnLysGluAla 1861 ::: :: 5447 GTCGTGAACATGTACATTGCCATCATCCTGGAGAACTTCAGTGTAGCCACAGAGGAAAGT 5506	ර සි
US-10-473-173-94 ; Sequence 94, Application US/10473173 ; Publication No. US20060088823A1 ; CENTERAL THOMBER TON.	sn	1822 TyrAsnThrVallleSerProlleTyrPheValSerPheValLeuThrAlaGlnPheVal 1841 :::	ò a
6101 GTCAGAGAATCCAAGTGTTAGAGGAGAA		1809 LysAspProSerArgAspCysAspGlnGluSerThrCys 1821 ::: 5327 CGCCCCCTGACTGCAGCCTAGATAAGGAACACCCCAGGGAGTGGCTTTAAGGGAGATTGT 5386	oy qa
· m •	a da	1794 ThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMet 1808 ::::::: 5267 TGCCTGTTTCAAATCACAACCTCAGCTGGTTGGGATGGCCTGCTGCTGCTGCTAAAC 5326	\$ 6 6
	d	1774 HisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeu 1793 ;:: ;: - - - - - - - - - - - - -	& A
5951 CTGGAGAATGGAGCACACACCGGGAGAAAAAAGAGA 2114 pAlaLysAspProProGluThrArgSerSerLeuGlu	음 -	:::	qa
2094 nSerLysValSerLysHisIleArgLeuProAlaPro	λο 	<pre>5102 TTTGCCTTAATGATGTCCTTGCCTGCCCTGTTCAACATCGGCCTTCTGCTCTTCCTGGTC 5161 1754 PhePheIlePheAlaAlaLeuGlvValGluLeuPheGlvAsoLeuGluCvsAsoGluThr 1773</pre>	අ

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	ATCTATGCTATTATAGGATTGTATTATTGGAAAAATGCACAAAACATGTTTTTTTT	ThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCys	International control of the post of the property of the post of	GInArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThr :::::: GAGAAGGCAAAAGCACGGGGAGATTTCCAGAAGCTCCGG	IleLeuarglysalaalaargargleualaglnvalSerargalaileglyva	SHISHISHISHISHISIYrHISLEUGIYASNGIYINTLEUARGVALFOARGALASELFI OGLUILEGINASPARGASPALAASNGIYSERARGARGLEUMETLEUPROPROPROSETTH

2216 rProProSerIleSerIleAspProProGluSerGlnGlySerArgProProCy 2234	2234 sSerProGlyValCysLeu	2245 oAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSe 2264 	2264 rProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMe 2284	2284 tAspPro 2286 : 5713 GTCCCCA 5719
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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
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OM protein - nucleic search, using frame_plus_p2n model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli	Sequence 3, Appli	Sequence 3859, Ap	Sequence 49, Appl	Sequence 51, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli
QI	US-09-426-998-4	US-09-426-998-3	US-09-949-016-3859	US-08-984-709A-49	US-09-398-522-51	US-09-404-650-1	US-09-935-541-1	US-10-425-800-1
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Sequence 3, Appli Sequence 3, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 3, Appli Sequence 1, Appli	equence 1, equence 1, equence 1,
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ALIGNMENTS

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Sequence 4, Application US/09426998
; Sequence 4, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: ERLANDER, MARK G.
; APPLICANT: ERLANDER, MARK G.
; APPLICANT: GALINDO, JOSE E.
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOC ID NO 4
; LENGTH: 7741
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
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US-09-611-257A-24 (1-2287) x US-09-426-998-4 (1-7741)

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1750 eGlyAspLeuGluC 1770 |||||||||||||| rGGAGACCTGGAGT 5275 .IleSerProlleT 1830 ||||||||||||||| |ATCTCGCCTATCT 5455 oLeuGlySerProP 1890 |||||||||||||| ACTGGGCAGCCCCT 5635 5215 1790 calaglualaglnc 1590 1650 4915 5335 SProGlyAlaProH 1910 HisteucysThrs 1610 ||||||||||||| |CACTTGTGCACCA 4795 eCysasnTyrileP 1 leargasnPheGlym 1 ||||||||||||| rcggaacttrggca 5

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Sequence 3859, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER FILE REFERENCE: CL001307

CURRENT PILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3859

LENGTH: 7405
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuli
STREET: 4250 Executive Square, Suite 70
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: BA COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION STEPHANIC L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (fc
TELEPHONE: (619) 450-8400
TELEPHONE: (619) 587-5360
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 7898 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: NO
ANTI-SENSE: NO
REAGMENT TYPE:
ORIGINAL SOURCE:
FRATURE:
FRAT
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4.3 Prokegser/Redubles/Prova.Nalser/Asser/Serfser/Inffill
6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B

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RESULT 6
US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; TENGRAL 1001
                                                                     erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT
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Mismatches:
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61.7%
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| TYPE: DNA
| ORGANISM: Homo sapiens
| FEATURE:
| NAME/KEY: CDS
| LOCATION: (192)..(6716)
| US-09-404-650-1
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Best Local Similarity:
Query Match:
DB:
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Ω	1644 CGGCACTACCAGCTGTGCCCGCAACATAGCCCCCTGGATGCG	1685	10
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>-	658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThr	yAlaCys 676	
Q	1731GATCCCGCCAGCTGC	rrgcreccag 1757	7
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>	737 LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAsp	aGluProSer 756	
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2199 ProLysLysLeuSerProProSer 2219 AspLeuLeuProSerSerGlnGluGlu 2145 1958 5575 AlaGluArgSerLeuGlyHisArgGly 1978 5608 LeuGlySerProPheLeuTrpProGly 1894 CysTyrSerValGluThrGlnSerCys GlyvalSerArgThrHisSerLeuPro SlnArgProleuArgArgGlnAlaAla GlyserArgGluAspLeuLeuserGlu AGATCCCAT------TCAACC GCAGTCAAGCACCCCCAAGTCCCTTCT ArgleuCysProSerProSerSerLeu rcecreaceccaecccaecae-crc ---HisProGluGluValProValPro |||| ::: ||| ::: :::||| CATCCTGCTGGTGACGACCTGAGTCT HisTyrLeuLeuGlnProHisGlyAla AspproProGluThrArgSerSerLeu ccareccaeccaerrerrecaecere | :::::||| | GCACTGGAACCCTCCCCAAGA ProGlyAlaProHisThrThrAlaHis |||||||||||| |CGGGCGCCCTGGCCGAGGGCCG---| | | | GCAAGAGGTGCAGCTGAGACGGA -------SGGTGAGCTGGACCCACCTGAGCCCAT SerSerPheTrpGlyGlySerSerlle ValSerLysHisIleArgLeuProAla :::||||||| seccectrerecceccecrecracrc LeuSerValHisSerGlnProAlaAsp crrer-deredecearereede ATGCCTCCAGCC------ProThrMetValPro-

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Matches:
Conservative:
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                                                                                                            Sequence 1, Application US/09935541; Sequence 1, Application US/09935541; Patent No. 6589787; GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VAR; TITLE OF INVENTION: T-TYPE Sequence listing CURRENT APPLICATION NUMBER: US/09/935,541; CURRENT FILING DATE: 2001-08-23; PRIOR APPLICATION NUMBER: 09/404,650; PRIOR FILING DATE: 1999-09-23; NUMBER OF SEQ ID NOS: 12;
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                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 6816
TYPE: DNA
CRGANISM: Homo sapier
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; NAME/KEY: CDS
; LOCATION: (192)..(6
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                                                                                                                                                                                                                                                                                                                                                            12 ThrProPrc
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rPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 	erGluHisGlnAspCysAsnGlyLysSerAlaSerGlyAr. ::: ::: CGGGCATGAGGACTGCAATGGCAGGATGCCCAGC	AlaargThrLeuargThrAspAspProGlnLeuaspGlyaspAspAspAspAspGlu ::: GCCaaagacGTCTTCACCAAGATGGGCGACCGCGGGGATGCGCGGGGATGAGGAA	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaC ::: ::	CysArgGluArgAspSerTrpSerAlaTyrIlePheProProGluSerArgPheArgLeu 	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe cTGTGTCAGACCATTATTGCCCACAAACTCTTCGACTACGTCGTCCTGGCCTTCATCTTT	LeuAsnCys1leThr1leAlaMetGluArgProLys1leAspProHisSerAlaGluArg 	IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal 	LysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn 	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer 	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 	ProbeuArgValileSerArgAlaGlnGlybeubysbeuValValGluThrbeuMetSer 	SerLeuLysProlleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly 	IlebeuGlyValGlnbeuPhebysGlybysPhePheValCysGlnGlyGluAspThrAr: 	AsnileThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr 	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly 	TrpValAspileMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet ::: :::	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhePhe
PheAspLeuProAspThrLeuGlnValPro GTGGACCTGGCCGAGCTGGTGCCCGCGT	AlaSerGluHisGlnAspCy gcccccggcargaggAcrc	ArgThrAspAspProGl 	LysGlyGluargIleGlnAl ::::: CTGTGCTTCCGCGTCCGCAA	AspSerTrpSerAlaTyrIl ::: GAAGACTGGTCTGTCTACCT	lleileThrHisLysMetPh ATTATTGCCCACAAACTCTT	ThrileAlaMetGluArgPr accarcGcccTGGAGCGGCC	LeuSerAsnTyrIlePheTh :::	LeuGlyTrpCysPheGlyGl crGGGCCTGTACTTCGGCGA	LeuLeuValLeulleSerVa TTTCTTGTCTTCGATCCAI	LyslleLeuGlyMetLeuAr 	eserArgalaGlnGlyLe 		GlnLeuPheLysGlyLysP} 	LysSerAspCysAlaGluAl ::: CGCTCGGACTGCATGGCCGC	LeuGlyGlnalaLeuMetSe 	MetTyrAspGlyLeuAspAl :::	TrpMetLeuLeuTyrPhel
182 SerPheAspLeu) 	202 SerSerAlaSerGlul :::::: 336 GCGGCAGGCCCGGCC	220 AlaArgThrLeu ::: 390 GCCAAAGACGTC	239 GlyAsnLeuSer) ::: ::: 450 ATCGACTACACCC	259 CysArgGluArg 510 TGCGAGGTCCGC	279 LeuCysHisArg 570 CTGTGTCAGACC	299 LeuAsnCysIle' 	319 IlePheLeuThr 	339 LysvalvalAla: :: 750 AAGGTAGTCTCG	359 ValLeuAspGly 	379 AspSerGlyThr: 870 GCCGGGGGAGCC	399 ProLeuArgVal 	419 SerLeuLysPro 	439 IleLeuGlyVal 	459 AsnileThrAsn 	479 AsnPheAspAsn 	499 TrpValAspile ::: 230 TGGGTGAACATC	519 AsnHisAsnPro

LeuaspGlualaLeuLysIleCysasnTyrIlePheThrValIlePheValPheGluSer ||||:::|||||||||||||||||||||:::||||||| crccacacccrcaagracTGCAACTATATGTTCACCACTGTCTTTGTGCTGGAGGCT LeuSerLeuProlleAsnProThrllelleArglleMetArgValLeuArglleAlaArg GCGGCCCTGCCCATCATCCGCATCATCGCCATCATCCGCATCATCGCGATCATCCGCATCATCGCGATCATGCCCGA ---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly 1679 1719 1579 5109

scccarsscririsscricisscricisscristraccisitrici

6179TGCCCT 2238 ValCysLeuArgArgArgAlaProAla ::: ::: 6218 CGGCCTGTCCCCGGCGCTCGCCGCG 2258 LeuAspSerThrAlaAlaSerProSer ::: 6278 GCGGGGCTGCGGGCGATCAGCGAG Sequence 1, Application US/10425800 Patent No. 6893842 3ENERAL INFORMATION: APPLICANT: Dietrich, Paul S. APPLICANT: McGivern, Joseph G. TITLE OF INVENTION: T-TYPE CALCIUM CHA TITLE OF INVENTION: AND USES FILE REFERENCE: R0043B-REG sequence li CURRENT APPLICATION NUMBER: US/10/425, CURRENT FILING DATE: 2003-04-29	prior Application Number: US/09/404,650 prior Application Number: US/09/404,650 prior Filing DATE: 1999-09-23 prior Filing DATE: 1999-09-23 prior SEQ ID NOS: 12 prior I LENGTH: 6816 prior TYPE: DNA prior Number (192) (6716) prior I Length: 192 (6716) prior I Length: 192 (6716) prior I Location: (192) (6716) prior I Location: (6716) prior I	.611-257A-24 (1-2287) x US-10-425-800-1 (1-6816) 12 ThrProProLeuArgGlySerAlaArgProSerSerAspP ::: 207 TCCCGCCCTCCTCATCTGCAGCAGCCCCAGCCGCTGAGC 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgArgN 267 CCCGGACCCCGG	Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65 Db 279AGCCCCCATCCTCCCGCCAGGCCTCTGGATGGAGCT326 Qy 66 AlaGlySerThrGluLySAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85 Db 327CATGTCCCACAC As DroAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105 Qy 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105 Db 345 CCAGACCTGGCGCCTATTGCCTTCTTCTGCTGCGACACACAC
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1575	AGC	1577
518	HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisTyr	537
1578	CGGCGCCAGGCCCTG	1592
538	HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp	557
1593		1601
558	AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly	577
1602		1628
578	ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro	597
1629		1643
598	ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly	617
1644	CGGCACTACCAGCTGTGCCCGCAACATAGCCCCCTGGATGCG	1685
618	SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys	637
1686	AGGCCCACACC	1697
638	AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnllePro	657
1698	CTGGTGCAGCCCATCCCCGCCACGCTGCTTCC	1730
658	ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys	929
1731	GATCCCGCCAGCTGCCTTGCTGCCAG	1757
	HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro	
1758	CATGAGGACGGCCGGCCCTCGGGCCTGGGCAGCACGGACTCGGGCCAGGAGGCCTCG	1817
697	AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal	716
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717	MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp	
1854	ĠÀTGGGĠÁĊGGGCCCGGAGCAGCAGĠĄĊGGAGCCTCCTCAGAA	1898
737	LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer	756
	SerValienAlaPheTroArdLeuileCvsAspThrPheArdLvslleValAsp	
1941	GTCTGGCTGTGCGGGGATGTGTGGCGGGAGCGCGAGCTGCGCGGCATCGTGGAC	2000
	SerLysTyrPheGlyArgGlyIleMetIleAlalleLeuValAsnThrLeuSerMetGly	
2001	AGCAAGTACTTCAACCGGGGCATCATGATGGCCATCCTGGTCAACACCGTCAGCATGGGC	2060
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835	TyrileLysAsnProTyrAsnilePheAspGlyValileValValileSerValTrpGlu :::::	854 2240
855	${\tt lleValGlyGlnGlyGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal}$	874

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 26 ProglyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAlaProArgSer
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Matches:
Conservative:
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                                                                                                   th, Paul S.
Th. Joseph G.
Th. T-TYPE CALCIUM CHANNEL VA.
TH. AND USES
O43B-REG sequence listing
NN NUMBER: US/09/404,650
FE: 1999-09-23
VOS: 12
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                                                                            on US/09404650
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                                                                 US-09-404-650-3

Sequence 3, Application US/
Sequence 3, Application US/
Batent No. 6309858

GENERAL INFORMATION:
APPLICANT: Dietrich, Paul
APPLICANT: McGivern, Josep
TITLE OF INVENTION: T-TYPE
TITLE OF INVENTION: AND US/
FILE REFERENCE: R0043B-REC
CURRENT APPLICATION NUMBER
CURRENT APPLICATION NUMBER
CURRENT APPLICATION OF 12
SOFTWARE: PatentIN Ver. 2.
SEQ ID NO 3
LENGTH: 6855
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (192)..(6755)
US-09-404-650-3
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Best Local Similarity:
Query Match:
DB:
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qq	1578CGGCGCCAGGCCCTG 1592		or MetherhenyelalaletheCa
ò	538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557	<u>`</u>	ά γ
DÞ	1593 1601	qq	61 ATGGACAACGTGGCCACCTTCTC
ò	558 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly 577	λo ·	915 LeuGlyMetHisLeuPheGlyCysLysPheAla
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ò	598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617	λ ^ε	954 ThrGinGiuAspirpAshLysValLeuTyrAsr
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ò	618 SerGlyLysValTyrProThrValHisThrSerProProRroGlulleLeuLysAspLys 637	λ (c	
ορ	1686ACGCCCCACACC	3 8	994
ò	AlaProSerProGlyProProThrLeuThrSerPheAsn	Zz dd	v د
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ò	<pre>erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys 6 :::</pre>	: q	72
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ò	677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696	7 A	78
qq	1758 catgaggacggcggcgccrtcggcraggcaccgacrcgacr	ò	044 SerLeuLeuProProLeullelleHisThr
ò	697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716	දු අධ	835 AGTCTCCCACTGGGTGGGCACCTA
qq	1818 GGCTCCGGGAGCTCCGCTGGTGGCGAGGACGAGGCG 1853	ò	060 HisProLysSerSerSerThrGlyValGly
ò	717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736	qa	886CCCCGACTCTCACTGCAGCCGGACCCC
q _Q	1854GATGGGGACGGGCCCGGAGCAGCGAGGACGGAGCCTCCTCAGAA 1898	ò	080 SerSerSerGlySerAlaGluP1
δ	LeuargaspProHisSerArgArgAndInArgSerLeuGlyProAspAlaGluProSer 756	qü	 943 AGTGTCATGTCTCTA
qq	CTGGGGAAGGAGGAGGAGGAGCAGGCGGATGGGGCG 19	ò	1100 AlaArgSerSerProHisSerProTrpSerAld
ò	SerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774	ପ୍	:::
අු	1 GTCTGGCTGTGCGGGGATGTGTGGCGGGAGACGCGAGCCAAGCTGCGCGCATCGTGGAC 20	δ	rLeuGlyArgAlaPro
S 4	775 SerLysTyrPheGIYArgG1Y11eMet111eAia11eLeuvalAsn1hrLeuserMetG1Y 794 [qa	3054 AGCTGGAACAGCCTC
3 2	voi adchadiaciichecadda chichida ichida chichecata chicheada a chicheada chi	δ	1140 ArgSerLeuLeuSerGlyGluGlyGlnGl
; 검	1 ATCGAGCACGAGGAGGAGGAGGAGCTGACCACATCTGGAATCTGCAATGTGGTC 21	qu	3096 GAGTCCTGCTCTGCGGAGCGCGGGCGCC
8 8	815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLvsLeuLeuValTvrGlvProPheGlv 834	ò	1159 GluAspArgAlaSerProAlaGly:
; a	1 Trcaccagcargttrgcccragaagatgarccraaagcragcracattraggcrctrcaac 21	qu	9
\ }	TyrileLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGlu 854	δδ	170
, do	:::::	අ _ධ	16 CCCCATCT
ò	855 IleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874	λ _ο α	1182 SerPheAspLeuFroAspInrLeuGINVAIFIG
QQ	gecrecrececer	} &	202 SerSer
ð í	875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894	ි දි 	336 GCGGCAGG
g	2301 CTGAAACTGGTGCGCTTCATGCCTGCCCGGCGCCCAGCTCGTGGTGCTCATGAAGACC 2380	_	

2540 -------AlaAlaThrProMetSer 1059 lualaLeuGlySerGlySerArgArgThr 1079
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TGCTGGTGGCCCTGGGCTCCCGAAAGAGC 2942 1099 :: CCCCACACGCCCACCATTCATCACGGG 3215 || :::||| |GCCGGACGCTGTCCCTCGACAACAGGGAC 3275 lyAspAlaThrLysSerGluSerGluPro 1013 -----AspGlyAsp 1023 ATAAGCTCCAGGAAGGCCTGGACAGCAGC 2780 luSerGlnAspGluGjuGluSerSerGlu 1158 rgGlySerLeuGluArgGluAlaLysSer 1181 973 ACATGCTCTTCATCTTCAGGATC laSerGluArgAsp---GlyAspThrLeu snGlyMetAlaSerThrSerSerTrpAla lyAsnTyrValLeuPheAsnLeuLeuVal laLeuGlyGluHisAlaGluLeuArgLys TGAGCTATGACCAGCGCTCCCTGTCCAGC laAlaSerSerTrpThrSerArgArgSer laHisHisGluMetLysCysProProSer GTCCTGCTGGGGCTGCGGGACCTGCC--erAspHis-----

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                                                                                                                                                                                                                                                             APPLICANT: Dietrich, Paul S.
APPLICANT: Dietrich, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/935,541
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 09/404,650
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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TYPE: DNA
ORGANISM: Homo s
FEATURE:
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; LOCATION: (192)
US-09-935-541-3
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                                                     ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu
                                                                                                                                                           SerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg
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---AspProGlnLeuAspGlyAspAspAspAsnAspGlu 1238 LysglyLysPhePheValCysGlnGlyGluAspThrArg GlyLeuAspAlaValGlyValAspGlnGlnProIleMet ArgileGlnAlaTrpValArgSerArgLeuProAlaCys TyrilePheThrAlaValPheLeuAlaGluMetThrVal ArgGluGluLysArgLeuArgArgLeuGluLysLysArg

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is Sequence 3, Application US/10425800

is Patent No. 6893842

is GENERAL INFORMATION:

APPLICANT: Districh, Paul S.

APPLICANT: McGivern, Joseph G.

TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

TITLE OF INVENTION: AND USES

TITLE OF INVENTION WINBER: US/09/404,650

PRIOR FILING DATE: 2003-04-29

CURRENT APPLICATION NUMBER: US/09/404,650

PRIOR FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 6855

TYPE: DNA

ORGANISM: Homo sapiens

PEATURE:

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Sequence 12, Application US/09404650
; Sequence 12, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
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Matches:
Conservative:
Mismatches:
Indels:
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Dp	594 GCAAGATCCTGCAGGTCTTCGATGACTTCATCTTCTTTTTGCCATGGAGATGGTGC 653	ò
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8	lallePheGlnVallleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspA 39	qa
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lyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleA
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                                                                                                                       CHANNEL VARIANTS; COMPOSITIONS
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                             RESULT 13
US-09-935-541-12
; Sequence 12, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: Dietrich, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VAR:
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VAR:
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VAR:
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; SOFTWARE: PATENTIN VOS: 12
; SOFTWARE: PATENTIN VOS: 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: RATTUS SP.
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	4 ACCGGCGCCAGGCC	ò	890 ValLeuMetLysT
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	58 laAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP 578	ζŎ	_
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	9 TCCAGAGCAGTGAGGATGGGGTCTCCTCGGACCTGGGGAAGGAGGAGGAACAGGAGGACG 19	qa	93
	750 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 769	<u>ک</u> و	1099 SerAlaArgSerSer ::: 3044 AGCTCCCGABCTCC
qq	1989 GGGCAGCCCGACTGTGTGGG-GATGTGTGGCGCGAGAAAAAAGCTG 2038	3 8	119
	770 ArgLyslleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaileLeuValAsn 789	qa Z	04 TCCAGCTGGAAC-
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	830 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 849	, c	

2818 2398 2458 2518 2578 2638 2698 1008 3103 1138 | SerGlyGluGlýGlnGluSer----GlnAspGluGluGluSer 1156 ----ArgHisArgGlySerLeuGluArgGluAla 1179 GCACACCGTCACCGACACCACCGCCGGACTCTGTCCCTTGATACC 3325 929 |||||||||||| |TCACTGCAGACCCGGTACTGGTGGCCCTAGACTCTCGGAAA |||| |GACCAGAGCTCATCCAATTTGGAGGAGTTTGACAAGCTCCCAGAG MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheile 1ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSer ArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu |LeuProProLeulleIleHis-----ThrAlaAlaThrProMet SerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArg 'SerAlaGluProGlyAlaAlaHisHisGluMetLysCysProPro CTG------GGCAGGATGAGCTATGATCAGCGATCCTTGTCC 111eValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPhe :----ccrcrdggrgcgcArcrgggrccrdcrggrAccArgggr AspPhePheSerProSerValAspGly-------AspargalaSerProAlaGlySerAspHis------

400 TTCTTTGTGCTCAACATGTTTGTGGCCGTGGTCGTGCAGAACTTCCACAAGTGCCGGCAG 445 557 HisGlnGluGluGluAlaArgArgArgG1uGluLysArgLeuArgArgLeuGluLys 157 460 CACCAGGAGGCTGAGGCGTGGAGAAACGGCTGCGCGCTGGAAAG 451 577 LysArgArgSerLysG1uLysG1nMetAlaG1uAlaG1nCysLysProTyrTyrSerAag 159 577 LysArgArgSerLysG1uLysG1nMetAlaG1uAlaG1nCysLysProTyrTyrSerAag 159 520 AAGCGCCGTAAGGCTCAGAGGCTGCCTACTATGCTACC 550 TyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPhe 161 61	ACTGTCCCACAAGGCTGCTCATCCATGTGCACCAGCCACTACCTGGACATCTT	57 GluservalPheLysLeuvalAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsn	SASDEROIDEILEAIGILEMELAIGVALLEUAIGILE 1717 [AACCCCACCATCATCGTATCATGCGTGTTTTGCGTATC 4910 LLYSMETALAVALGIYMETAFGALALEULEUHISTDEVAL 1730 [ABAGATGGCCACAGGAATGCGGGCCCTGCTGGACACAGTG 4970	3.7 MetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheFheile 175	777 GluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPh :::	TGATGAGCGCACGTGCCTAAGCAGCTTTGTGTCACCGCTCTTTGTGAGC 527. TGATGAGCGCACGTGCCTAAGCAGCCTGCAGTTTGTGTCACCGCTCTTTGTGAGC 527. EVAlleuThrAlaGlnPheValLeuValAsnValVallleAlaValLeuMetLySHis 185.	339 CTGGATGACAGCACAAGGAGGCCCAGGAGGATGCAGGATGCTGAGATCGAGCTG 539 874 GluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro 189
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Qy 2212 LysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArg 2231 :::	RESULT 14 US-10-425-800-12 i Sequence 12, Application US/10425800 j Patent No. 6893842 j GENERAL INFORMATION: j APPLICANT: Dietrich, Paul S. j TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF; j TITLE OF INVENTION: AND USES j FILE REFERENCE: R0043B-REG sequence listing j CURRENT APPLICATION NUMBER: US/10/425,800 j CURRENT FILING DATE: 2003-04-29 j PRIOR APPLICATION NUMBER: US/09/404,650 j PRIOR APPLICATION NUMBER: US/09/404,650 j PRIOR PILING DATE: 1999-09-23 j NUMBER OF SEQ ID NOS: 12 j SOFTWARE: PatentIn Ver. 2.0 j SEQ ID NO 12 j LENGTH: 6503 j TYPE: DNA	ORGANI 10-425- Jument 1. No.: Cent Si I Local FY Matc	Db 64 ccccccccccccccccccccccccccccccccccc	234 TCCATGCCAAGGGCTCCCTGCTGACATGGCTGACAGCAACTTACCGCCCTCAT 57 rCysProGlyProGlyAlaAlaGlyAla-GlySerThrG
5405GCCCATGGCCTCGGCCCCTGGCCCTGGT	5516 C 1967 - 1986 S 5609 A 2006 P 5669 T 5669 T 5729 A	5789 2051 2069 5909 2089 5955	6015 GCTCCAGCCTCTCTGTAGATGCCTGCTGAGTTCTTCCACCCTGCTGTGCCAGCC 2106	
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Dp	59 ATCTGCAATGTGGTCTTCACCAGTATGTTTGCCCTGGAGATGATCCTGAAACTGGCCGCC 22	ζó	1170
	#30 TyrGlyProPheGlyTyrileLySAShProTyrAshilePheAspGlyValileValVal #49 :::	qa	· ·
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	9 PheAsnLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLys 100	qa ——	3740 GAGCGCATC
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	1041 LeuArgLysSerLeuLeuProProLeullelleHisThrAlaAlaThrProMet 1058	÷ €	3977 VAISELASE 3920 GCCTCTGC
	2879 CTGGACCCTAGCCTCCCTCTGGGTGCGCATCTGGGTCCTGCTGGTACCATGGGT 2932	} &	397
	9 SerHisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArg 107 :::	. 음	σ
	29	ò	1417 MetSerSe
	9 ThrSerSerSerGlySerAlaGluProGlyAlaAlaAlaHisHisGluMetLySCysProPro 10	qa	4040 ATCTCCTCC
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	SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg 111	අ ධ	4100 TTCGGCATC
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aArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAspAsn alLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMet SINIBETH AS SOLVES DE CYSALAGIUA LA SENTY PARGINA VALANGHIS SOLVE LE SOLVE rPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer

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	7	
2192 LeuCysProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgPro 221	9740 CAGCTCC	AGCCTTGGCCAGCTGTTTCC97
6269	01 ArgProA	pCysLeuArgThrValCysAsnProTrpPheGluArgValSerMet 120 :::
Qy 2212 LysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArg 2231	DD 9767	CCTGGTTTGAGCGCATCAGCAT
Db 6323 CGGCTAGCCTGTCACCGGCCACCCCGGCGCCGCCTCAGCCTGCGGGGCCGTGG 6376	uVa !	eLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluA
ProCysserPro-GlyValCysLeuArgArgArgAlaProAl	Db 9803 TIGGICA	
Db 6377 CCTGTTTAGTCTGCGTGGGGGCCCATCAGCGTAGCCACAGCAGTGGCGGCTCCAC 6436	Asps	erGlnArgCysArgil
Qy 2248AspSerLysAspProSer 2253	 Db	
Db 6437 CAGCCCTGGCTCCACCACGACTCCATGGACCCCTCT 6476	. Qy 149	149
RESULT 15	Db 9923 GTGTTGT	GTGTGTTGGGGGTTGGCCCCTCTTAATCTTAATACCCTCTACTCCTCTGCAAG 9982
US-UV-949-U16-156U1 ; Sequence 156U1 Application US/09949016 ; Botton Mo 5013330	Oy 149	149
FACCIL NO. SOLESSY. FACTOR NO. SOLESSY. FACTOR FORMATION:	Db 9983 AGGCCCT	GACCCAACTGGTGGGACTAGGGTGGGACTAGAGGGTATTCCCTCACCCACGT 10042
; AFFLICANT: VENIEK, V. CIGIY GE GI.; ; TITLE OF INVENITON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED . TITLE OF INVENITON: WITH HIMAN DISEASE METHODS OF DETECTION AND HERS THEREOF	Qy 150	
TICKEN DISEASE, MEINOUS OF DEIECTION AND OSESS	Db 10043 CTCAGTTT	CAGCCACCTCTTGTCCCCACATCAGGCCTTTGATGACTTCATCTTTGCTTC 1
02/03/343,01 04-14 0/241,755 20	Oy 160 PheAlaV	ValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyr 179
; PRIOR APPLICATION NUMBER: 60/237,768 ; PRIOR FILING DATE: 2000-10-03 : PRIOR APPLICATION NUMBER: 60/231,498	Oy 180 LeuGlyA	.I.le
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; SEC ID NO 15601 ; LENGTH: 70308	Db 10223 CTGGGGT	GGGAGAGCAATGGATCAGATCGGTCCCTTCCCCGGGGCCAGGGTTCTGGGCCT 10282
; IIFE: DNA ; ORGANISM: Human !X-09-49-016-15601	Oy 193	193
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Qy 18 SerAlaArgProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThr 35	93 -	193
9539 TTGTCTTTACAGATGAGGAAGCTGGGTCCAGAGAGGTGAGATGACC	23 CCTGCTG	CCCCTAAAGCAGGATTCCTCATTGACCTCTTGTGACCCCCACTGTGGCCTCAGA 10
Qy 36 ArgArgAetGluArgAlaProArgSerArgAspSerProValAlaSerArgSer 54	194	AlaGlyMetLeuGluTyrSerLeuAspLeu 203
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Db 9623 GGGCTGGGGCTGCTGCGTGTATGTCAGGGCCCTGGCACCACCTGCTTAGCCT 9679	224	ProSer 228
70 GluLysAspProGlySerAlaAspSerGluAla 80 ::: ::	1070	 3cccagtgagtgacccctcagccctcagcccctgaagagagccccaggagga 10
Db 9680 CAGATGGAGCCAGGAGGTAAACGAGGAGGAGGTGTTAGGGCGGGGTCGGGGGCCGGCC	Qy 228	228

10822 CCGTCAGGAACTCTCAGACCCCACTCTACTACTGTGTCCTCACCTGAACCCCTCACAGGCC 228 110822 CCGTCAGGAACTCTCAGGAAAACCCCACTCTCTCTCATTTTAGCTCTGCATTTAGGTCAG 228 111022 GAGGCACTATGGAAGTTACCTGGAAAACCCCACTCTTTTAGCTCTGGCTTTAGGTCAG 228 111022 GAGTAGGGGTGTGGGGAATGACCCTCTTCTTCATTCAGTTAGATGACTCCCCCAGGA 228 111022 CCGTTTTCTAGGAAACATCTCAGAAGACCCTCTTCTTCAGTTAGATGACTCCCCCCAGGA 228 111122 CCACGCTGAACGTTCTCCAGAAGACCTCTTCCTTCAGTTAGATGACCCTCTCCCCCCAGGA 228 111123 CCACGCTTCCTCCTTCCTCAAGACCTCTTCCTTTCAGTTAGTT
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13042 CGGTTGCTACTGACATATCTGATCTGAGACATATCTGGTTCTCAAACTTGGCT 13101 281 13102 ACCCATTGGAACCACCTGGGGAGTTTTAAAAAGTACTGATGCTGGGGGGCCCCCCGGA 13161 281 1322 GTGATCCTGATTTCATTGCTCTGGGGCTCAGCTTGGATGTTTTTTCAACCCCTCCAGA 13161 281 1322 GTGATCCTGATTTCATTGCTTGGGGGTTTTCAAAATTTCAAAGTTTTTCAACCCCTCCAGA 13161 281 1322 GTGATCCTGATTTCATTGCTTGGGGGTTTTTTCAAAGTTTTTCAACCCCTCCAGA 13161 281 1324 CCTGAGTCTGGAGTTTCCCCACTCAGGCCTCAGGTGGCCTTCCAGCATTTTTCAACCCTCCCT	14061 CCCCGGGGGGATGGGGGGATGCTGGGGGGGGGGGGGGTAGTT 1412
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) E	GGACTTCTTTGTTGTTGAGGTTCAGAGAGAAATTGTTGTTGTTGTTGTTGTTGTTCAGCTTTCATGAGCTT	Db 18801 AAGGGGAGGCTCCTTGCTGAAGGCACCTAGGATATAGGAGCTGTCCAGGACCTCAG 18860
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Š i		Db 18861 AGGACATCCAGGCCACCTCTCTGAGCCCCAGGACACTCAGCAGTGACTGTCAATGAAGTG 18920
qq	CCACTGGCTAAACCTGAGTCTCATTGCCTCCGCACAGGGAGACCCAGTTCAGGGAGCTGC	Qy 673 673
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qq	17841 TTGTCTGATGGGTGACACTCCCAGTGTGGGGGCAGTGAGACACATAGGGACGTCGGG 17900	Oy 673 673
ò	673 673	18981 CCTGGCCCACTAAGTGCCTAGCACCCCATCACTGTAACAACCCCAGACTCCCTGACTCAT 19
QQ	17901 CTCTCCCCAGCAGACAGGTTCACTGTAGCTGCAGGCCCACGGCCTGTGTTTCAGGAAGGA	673
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Ωp	18021 CCAGAAGGTGCTATCACAGAACCCAGAGCGAAAGGTTTCTATGCCAGGTCCCTCCACTACC 18080	000 3:00=[83:[334Ebake=[8050305:1750505050505050505050505050505050505050
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ò	673 673	19221 GAGGTGGAGCTCGCCGACGTGAAATGCCTGACTCAGACAGCGAGGCAGTTTATGAGTTC 19
qq	18141 GCAAGGCTGGGCCCATAATTACTCTCAGTGGTGCTTACTGACTCCCTCC	729 ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSer 748
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	829 ValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal 848	548GGGCCTTCTACCTCCCTCCTCCTCTCAGCTTCCTCCATG 19601	849 ValileSer-ValirpGluileValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgTh 868	CTGCTAGCCCACCTGGCAGGTAGGAGGTGGTGGTAGCAATGCATGG 19655	868 rPheArgLeuMetArgValLeuLysLeuValArgPhe	656 GGATTCTCTAGAGGGAGTGCTTAAAGTCTCTGAGTATGGAGGTCGCCTCAGGTAGGCCAC 19715			Search completed: July 10, 2006, 07:21:54
	ValTyrGlyProP	GGGCCTT	VallleSer-Val	CTGCTAGCCCACC	rPheArgLeuMet	GGATTCTCTAGAG		AGGGTATGTTCTA	ed: July 10,
19515	829	19548	849	19602	898	19656	881	19716	h complet
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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-Q=/abss/ABSSWEB spool/US09611257/runat 10072006_064126_6972/app_query.fasta_1
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-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-WAXLEN=2000000000 -HOST=abss06p
-USER=US09611257 @CGN 1 1 7492 @runat 10072006 064126_6972 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Sequence 9; Appli
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US-10-425-800-3

US-10-425-800-12

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US-10-033-026-5

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US-10-377-139-7

US-10-930-301-51

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GENERAL INFORMATION:
APPLICANT: MacKinnon, Roderick
APPLICANT: Jiang, Youxing
APPLICANT: Lee MacKinnon, Alice
APPLICANT: Ruta, Vanessa
TITLE OF INVENTION: Voltage Sensor Domains of
FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
CURRENT APPLICATION NUMBER: US/10/377,139
CURRENT FILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
 TYPE: DNA
ORGANISM: Homo sapiens
SEQ ID NO 10
LENGTH: 7648
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Length: Matches:

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Alignment S Pred. No.: Score: $^{\circ}$

1 GlyTyralaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 36 1 GlyTyralaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 36 1 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACGCTGGAGGGCTGGGTCGACATCATG 10 1 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 38 1	1 Inrivistinargiciuserginiceumecargiciusinargivalarginiceuserasinara 12	1	1 HishishishishishudlyasnGlyThrLeuargalaProArgalaSerProGlu 5	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	581 GlyargThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600	21 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 64	61 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGly
8 8 8 8 8 8	8 8 8 8	8 6 8 6 8	8 6 8 6	6 6 6 6	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	8 6 6 6	6666
Percent Similarity: 95.3% Conservative: 1 Best Local Similarity: 95.2% Mismatches: 1 Query Match: 99.3% Indels: 111 BB: 2 US-09-611-257A-37 (1-2266) x US-10-377-139-10 (1-7648) Qy	Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60	241 CCCTGGTTTGAGCGCATCAGCATGTTGGTCATCTTCTCAACTGCGTGACCCTGGGCATG 30 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 12	361 GATGACTTCATCTTTGCCTTGGCGTGGATGGTGGTGGTGGTGGCCTTGGGC 4 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 1	22 60 24	221 ValPhePheilePheGlyileValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 24	721 TGCTTCCTACCTGAGAATTTCAGCCTCCCCTGAGCGTGGACCTGGAGCGCTATTACCAG 78 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 28	Db 841 TCCTGCAGAAGCGTGCCCACGCTGCGGGGGCGGTGGCCCCACCTTGCGGTCTG 900 Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320

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Scantiago, Inmaculada

asof, Scott D.

ION: METHODS AND COMPOSITIONS FOR TREATING

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ION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,

ION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,

ION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,

ION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,

ION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,

ION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,

ION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR

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Mismatches:
Indels:
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Matches:
PRIOR FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/471,614
PRIOR FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US 60/478,742
PRIOR FILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/499,529
PRIOR FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US 60/499,594
PRIOR FILING DATE: 2003-09-02
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CRGANISM: Homo sapiens
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APPLICANT: Aziz, Nata; APPLICANT: Zlotnik, JITLE OF INVENTION: NO. TITLE OF INVENTION: FILE REFERENCE: file CURRENT APPLICATION NO: CURRENT FILING DATE: NUMBER OF SEQ ID NOS: SOFTWARE: Patentin vei; SEQ ID NO 31
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TYPE: DNA
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; APPLICANT: WANG, JAW-YUAN
; TITLE OF INVENTION: GENES FOR DIAGNOSING COL;
; FILE REFERENCE: BHT/3230-85
; CURRENT APPLICATION NUMBER: US/10/786,148
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 120
; LENGTH: 7825
; TYPE: DNA
; ORGANISM: Homo sapiens
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RESULT 4
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; Sequence 120, Application US/10786148
; Publication No. US20050191634A1
; GENERAL INFORMATION:
; APPLICANT: LIN, SHIU-RU

621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640 [681 AlaAspArgGluMet ProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700	721.GlubroSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740	761 GlylleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780	801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820	841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860	881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900	921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940	
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WATION:

Dring, Jeanne F.; Kaser, Matthew R.

ENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS

CE: PA-0026-1 CIP

ICATION NUMBER: US/10/062,674

NG DATE: 2002-01-30

ATION NUMBER: US 09/625,102

BATE: 2000-07-24
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SOFTWARE: PERL Program
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LENGTH: 8116
TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
CTHER INFORMATION: Incyt.
FEATURE:
NAME/KEY: unsure
LOCATION: (1) ... (8116)
COTHER INFORMATION: a, t, US-10-062-674-2011
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Query Match:
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; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7129
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; ORGANISM: Rattus Sp.
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; Publication No. US2003
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T
; FILE REFERENCE: 004.0
; CURRENT APPLICATION N
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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; LOCATION: (373)...(3993)
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Query Match:
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6822 AAAGACACGCTGAGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 6875
                                                                                                                                                                                                                                                                                                                                                                                                                      gene encoding a T-type calcium channel
                            RESULT 9
US-10-930-301-51
Sequence 51, Application US/10930301
Publication No. US20050026207A1
GENERAL INFORMATION:
APPLICANT: Issa, Jean-Pierre
ITTLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: JHU1590
CURRENT APPLICATION NUMBER: US/10/930,301
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 3993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3993
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: McManus, Owen APPLICANT: Garyantes, Tina APPLICANT: Garyantes, Tina APPLICANT: Bennett, Paul B., Jr. APPLICANT: Imredy, John P. APPLICANT: Bugianesi, Randal M. APPLICANT: Bugianesi, Randal M. TITLE OF INVENTION: ELECTRICAL FIELD STIMULATION OF TITLE OF INVENTION: ELECTRICAL FIELD STIMULATION OF TITLE OF INVENTION: EUGRAYOTIC CELLS FILE REFRENCE: 20794YP CURRENT APPLICATION NUMBER: US/10/483,467 CURRENT FILING DATE: 2001-01-12 PRIOR APPLICATION NUMBER: 60/304,955 PRIOR APPLICATION NUMBER: 60/304,955 PRIOR FILING DATE: 2001-07-12 NUMBER OF SEQ ID NOS: 12 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 7898 TYPE: DNA US-10-483-467-3	Alignment Scores: Pred. No.: Score: Score: Fred. No.: Score: Fred. No.: Score: Fred. No.: Fre	US-09-611-257A-37 (1-2266) x US-10-483-467-3 (1-7898) Qy 7 GlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMetArgLeuAsnAspLeuSer 26	37AlaGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAl 410 GGCGCCGAGCGCGCGGAGCTGGCTGCCGAGGAGCAGCGCGTCCCGTACCCGGC 55 aLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLe 11	530 CCGCCTGCTCCCATGCTTCGAGCACGTGAGCTAGCTGCTAATTCGAGCTCAACTG 58 95 sValThrLeuGlyMetPheArgProCygGluAspIleAlaCygAspSerGlnArgCysAr 11	aValGluMetValValL GGTGGAGATGGTCATCA GGTGGAATGGTCATCA YASPThrTrpAsnArgL TGACACGTGGAACAGGC uAspLeuGlnAsnValS	
	1021 3364 1041	Oy 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080		1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	Db 3844 CCAGGGCTGCATCGCATGGCCGAGGGTCTGCTTCTGAGCACCAGGACTGCAAT 3903 Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220 Db 3904 GGCAAGTCGGCCTTCAGGCGCCTGGGGCCTGATGACCCCCCACTGGAT 3963 Qy 1221 GlyAspAspAlaAspAspGluGlyAsnLeu 1230 Db 3964 GGGGTGACGCCGATGACGAGGCAACCTG 3993	RESULT 10 US-10-483-467-3 ; Sequence 3, Application US/10483467 ; Publication No. US20050164161A1 ; GENERAL INFORMATION: ; APPLICANT: Kath, Gary S.

 1931 CCCAGGCCGCGG	62		580 rGlyArgTh	51	594	2111 GGGCAGCGGCAA	599 oGluThrLeuLy	111 AGGCACC	619 uThrSerLeuAs		639 nSerThrGlyAl	2249 TGGACTGGGCCA	652 rProCysLeuLy	2309 CCCCCC	672 gAlaGlyAl	1 2363 TGCCCTGGAGG	691 uAlaValTyrG	 2423 TGGCGTCTATG	604	2483 ACCCCGTGCGA(715 rLeuGlyProAs	2543 GAGGGCAGCCC	735 rPheArgLysi	2603 GCTGCGCCGCA	755 lAsnThrLeuS	2663 CAACACGCTGA	775 uGluileSerA	2723 GGAGATCAGCA	795 uValTyrGlyP	1111 2783 GGCCTGCGGCC	815 lvalileSerV	2843 GGTCATCAGCG	835 rPheArgLeuM	2903 CTTCCGGCTGC	855 uValValLeuM	
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SerLysAspProLeu-----AlaSe 2235 ||||| :::||| crccregagcccacagaggccrcaggcgccccg 6970 ----AlaSerProSerProLysLysAspValLe 2252 LeuGlyGlyGlnProLeuGlyGlyProGlySe 2189
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::||| ...--GlylleCysLeuArgArgAlaPr 2225 ThrGluLeuSerTrpIleSerGlyAspLeuLe 2118 | |||:::::::||||| ||| :: GlualaginSerCysGlnArgArgProThrSe 2149 6691 2043 6361 ProLeuAlaArgAlaTyrSerPheTrpGly-- 2060 GlyProGluProAsnTrpGlyLysGlyProPr 2098 ::: GCGGAGCTGGGCAGCGGGAGCCTGGGGAGGC 6751 6028 2025 |||::: |ccdergacccagggggggcrccrccaggrcccc 6421 sigereccidicirceececcicacccccccc 6088 AspThrSerTyrIleLeuGlnLeuProLysAs 1987 AlaProThrTrpGlyThrIleProLysLeuPr 2007 GGCGGCACCACACTGAGGCGCAGGACCCC SerileThrileAspProPro---GluSerGl AlaGlnArgProLeuArgArgGlnAlaAlall IleAlaValSerCysLeuAspSerGlySerGl CTCAGCCGGCTGCTCTGCAGACAGGAGGCTGT LeuGlySerArgGluAspLeuLeu----Al glyTrpglyLeuProLysAlaGlnSerGlySe dedeccederaccec-----rregecre GAGTCCTGTCCTCCAGATCCCA----3lySerThrAlaGluGlyPro-Glyglngluglubropro-|||| |GGCGGAGAG------

13 ACACTGCCCATGCTGCTGCTGCTTCTTTTTCTTCTTCTTCTTTTGGC 67 13 ACACTGCCCATGCTGCTGCTGCTTCTTTTTTCTTCTTCTTCTTTTGGC 67 27 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 24 27 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 24 28 ATCATAGGTGTGCGTGGGGGGCTGCTGCTGCTGCTTCCTTC	nrCysValAsnTrpAsnG1 ::		LeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 45 :::	99 HisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAla 41 GCCAAGGAGCCCCGGCACTACCATGGAAGACTAAGGTCAGGA 16 ArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMet 1
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Db 6971 GGGGACCCTGCAGGCGAGGGGAGCCTGGGGCCTCCTGCCGGGCTGAGCACCT 7030 Qy 2252 uSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266	; SOFIWAKE: Facencin Version 3.1 . ; SEQ ID NO 8 ; LENGTH: 6990 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-377-139-8 Alignment Scores: Pred. No.: 5496.50 Matches: 1244 Percent Similarity: 60.3% Conservative: 216 Best Local Similarity: 51.4% Mismatches: 525 Query Match: 46.2% Indels: 437	9 Gaps: 7 (1-2266) x US-10-377-139-8 (1-6990) 9ProGlyProGlySerAlaGluLySASpProGlySerA:	87 SerMetLeuValileLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 10 [Db 373 TTCTTTGCCATGGAGTGGTGCTCCAGGTGGTGGCCTTGGGATTTTTGGCAAGAAGTGC 432 Oy 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheileValileAlaGlyMetLeuGlu 166

3211 GTGCCCGCGGTGGGCCCCCCCGGGCCGCCTGGAGGCCG 1196 HisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAla 1196 HisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAla 3271 CATGAGGACTGCAATGGCAGGAT-GCCCAGCATCGCCAA 1216 AspProProLeu-AspGlyAspAspAlaAspAspGluGlyAs 1216	do yo	OY OF THE CONTROL OF
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1076 GluProGlyAlaAlaHisGluMetLysSerProProSerAlaX ::::::: :: 2869 CTAGGGAGGATGAGCTATGACCAGCGCTCCCTGTCCAGCTCC	ζο Qα	1849 GGGGCGGICIGGCIGIGCGGAIGIGIGIGGGGGGAGACGCGAGCCAAGCCGAGCCAAGCTGCGCGGAACACAGCGAGCCAAGCCAAGCAGCGGGGAACACAGCGGGGAACACAGCGGGGAACACAGCGAGCAACACAGCGAGCAACACAGCGAGCAACACAGCGAGCAACACAGAGAGAACAGCGAGCAACACAGAGAGAGAGAGAACAGCGAGCAACACAGAGAGAACAGCAG
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laargalaLeuArgProasp 1215 AsnLeuSerLysGlyGluAr 1235 rgSerLeuLeuserGlyGlu 1135 ||||||||||||| AGTCCCTGCTCTCTGCGGAG 3030 ----GlySerAlaSerGlu 1195 cescadeccedecccese 3270 AAAGACGTCTTCACCAAGAT 3326 aArgSerSerProHisSer 1095 SCCATCTGGCGCACCGCCAC 3150 euglyProAlaSerArgArg 1068 ||||||||| |gGGACCTGCCCCCGACTC 2808 rArgashSerLeuGlyArg 1115 -SerSerSerGlySerAla 1075 2604 GTTTGATAAGCTCCAGGAA 2679 uValSerLeuGlyGluHis 1028 sThrAlaAlaThrProMet 1048 eSerLysArgGluAspAla 978 ::: :AAAGAGCAGTGTCATGTCT 3CTGGAAC-----

595 uAspLeuPheIleThrGlyValIleGlyLeuAsnValThrMetAlaMetGluHisTy 161: : :		7 80 7 80	1735 uPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluTh 1755	1775 uThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuAr 1795	1812 rPhevalSerPhevalLeuThrAlaGlnPheValLeuValAsnValIleAlaValLe 1832	1852 uLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerPr 1871		:::
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3327 GGGCGACCGCGGGGATCGCGGGGAATCGACTACACCCTGTGCTTCCG 3386 1235 gValArgAlaTrplleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSe 1255	1295 tGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTy 1315	135 374 137	yMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAl 1339	eValValileCysCysAlaPhePheileIlePheGlyIleLeuGlyValGlnLeuPheLy 143 ::	salaGlualaserTyrargTrpValargHisLysTyrasnPheAspAsnLeuGlyglnal 147	YeadspalavalGlyValAspGlnGlnProlleMetAsnHisAsnProTrpMetLeuLe	4227 GTACTTCATCTCCTTCCTGCTCATCGTTTTGTGCTCAACATGTTTGTGGGTGT 4286 1535 IValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluGluAlaArgArgAr 1555	1555 gGluGluLysArgLeuArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTy 1575

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Sequence 609, Application US/11000688

| Sequence 609, Application No. US20050287544A1
| Publication No. US20050287544A1
| GENERAL INFORMATION:
| APPLICANT: HOULGATTE, Remi
| APPLICANT: HOULGATTE, Remi
| APPLICANT: BIRNBAUM, Daniel
| TITLE OF INVENTION: GENE EXPRESSION PROFILLING OF COLON CANCER WITH DNA ARRAYS
| FILE REFERENCE: 1423-R-03
| CURRENT APPLICATION NUMBER: US/11/000,688
| CURRENT APPLICATION NUMBER: US 60/525,987
| PRIOR FILING DATE: 2003-12-01
| NUMBER OF SEQ ID NOS: 1596
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 609
| LENGTH: 6990
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OTHER INFORMATION: calcium channel,
OTHER INFORMATION: subunit (CACNA11)
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ORGANISM: Artificial Sequence
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US-09-935-541-3

Sequence 3, Application US/09935541

Sequence 3, Application US/09935541

Sequence 3, Application US/09935541

GENERAL INFORMATION:

TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THERE

TITLE OF INVENTION: T-TYPE Sequence listing

CURRENT APPLICATION NUMBER: US/09/935,541

CURRENT FILING DATE: 2001-08-23

PRIOR APPLICATION NUMBER: 09/404,650

PRIOR APPLICATION NUMBER: 09/404,650

PRIOR APPLICATION NUMBER: 09/404,650

PRIOR APPLICATION NUMBER: 09/404,650

SEQ ID NOS: 12

SEQ ID NO 3

LENGTH: 6855

TYPE: DNA

ORGANISM: Homo sapiens

FATURE:

NAME/KEY: CDS

LOCATION: (192)..(6755)

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Length:
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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Published Applications NA New:*

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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:* Database

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Sequence 31661, A Sequence 56474, A Sequence 3, Appli Sequence 7, Appli Sequence 9, Appli Sequence 9, Appli Sequence 13, Appli Description US-11-266-748A-31661 US-11-266-748A-56474 US-11-350-336-3 US-11-350-336-5 US-11-350-336-7 US-11-350-336-9 US-11-313-450-9 US-11-313-450-9 SUMMARIES DB 7834 8079 7364 7177 7011 6051 Length % Query Match 98.2 52.3 15.0 14.9 14.5 13.4 11684.5 6230.5 1786.5 1782.5 1776 1728.5 1678 Score 42643978

Sequence 56579. A Sequence 29006, A Sequence 11, Appl Sequence 104, App Sequence 104, App Sequence 104, App Sequence 103, Appl Sequence 111, App Sequence 101, App Sequence 101, App Sequence 152, Appl Sequence 152, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 9, Appl Sequence 9, Appl Sequence 9, Appl Sequence 9, Appl Sequence 92, Appl Sequence 92, Appl Sequence 96, Appl Sequence 118, Appl Sequence 1 US-11-266-748A-56579 US-11-266-748A-5006 US-11-266-748A-57267 US-11-266-748A-57267 US-11-263-326-98 US-11-263-326-104 US-11-263-326-104 US-11-263-326-148 US-11-263-326-149 US-11-263-326-149 US-11-263-326-146 US-11-263-326-101 US-11-263-326-101 US-11-263-326-101 US-11-263-326-101 US-11-263-326-101 US-11-263-326-101 US-11-263-326-101 US-11-263-326-101 US-11-263-326-90 15995.5 15996.1 15996.5 15996.5 15996.5 15596.

ALIGNMENTS

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RESULT 1
US-11-266-748A-31661

Sequence 31661, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT APPLICATION NUMBER: ED 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2005-03-14

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Conservative:
Mismatches:
Indels:
Gaps:
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; ORGANISM: Homo Sag
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Conservative:
Mismatches:
Indels:
Gaps:
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PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
SOFTWARE: Patentin version 3.3
SEQ ID NO 56474
LENGTH: 8079
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US-11-266-748A-56474
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                                                                                                                                                       TYPE: DNA ORGANISM:
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55815-0102 (319189)
FION NUMBER: US/11/266,748A
DATE: 2005-11-03
ON NUMBER: EP 041054926
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; APPLICANT: Harkin, P
; APPLICANT: Muligan
; TITLE OF INVENTION:
; FILE REFERENCE: 5581
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0 11 0 11 0 4	1130 CCGAGACAACC 291 pGlyGlyGlyG 1185Serf 307Serf	324 rAlaGlyGlui 1292 CTCGGGTGAC' 344 pIleAlaIlei 1352 GATTGCCATC' 364 tASPAlaHisi 1412 GGACGCCCAC'	384 ePheMetile 1472 CTTCATGATC 404 gGluSerGln 1532 GGAGAGTCAG 424 aSerPheSer 424 aSerPheSer 1592 CAGCTTCTCC 1592 CAGCTTCTCC	
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λλ	isLeuLeuGl 1993
qc	40 iccecccecadagrecrerecercecrecadarecarregerer 618
λζ	3 nProHisSerAlaProThrTrpGlyThrIleProLysLeuProProProGlyAr 201
qc	624
λ̈́ζ	011 gSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAs 203
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Dp	38 CAGCGIGGAIGCICAGGGCIICCIGGACAAGCCGGGCCGGGCAGACGAGCAGIGGCG 66
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Tue Jul

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RESULT 3
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; Sequence 3, Application US/11350336
; Publication No. US20060135751A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CH;
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/11/350,336
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FASELSEQ for Windows Version 3.0
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; TENACH:
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; Sequence 7, Application US/11350336
; Publication No. US20060135751A1
; GENERAL INFORMATION:
; APPLICANT: Schorge, Stephanie
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THER
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THER
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; PRIOR FILING DATE: 2001-12-28
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1999-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7-7-7
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477 Gl 1376 TC 497 Hi 1435 517 Al	Qy 537 ProSerThrProAlaLeuSerGly Db 1465	Db 1465	677 1544 697 1564 717	Qy 737 ArgLys1leValAspSerLysTyr Db 1571 CGGCGCATGGTGAAGGCTCAGAGC Qy 757 ThrLeuSerMetGly1leGluTyr Db 1631 ACACTGTGTGTGGCCATGGTGCAT Qy 777 IleSerAsnIleValPheThrSer Db 1691 TTTGCAGAGTTTGTTTTCCTGGGT Qy 797 TyrGlyProPheGlyTyrIleLys Db 1751 CTGGGGCCCAGAAGCTACTTCCGG Qy 817 IleSerValTrpGluIleValGly Qy 817 IleSerValTrpGluIleValGly Db 1811 GGGAGCGTCTTTGAAGTGGTCTGG
506 GGGACAAAACGCCCATGTCCGAGCGGTGGACGACGGAGCCCTATTTCATCGGGATC 565 128 PheAlaValGluMetValValLySMetValAlaLeuGlyIlePheGlyLySLySCys 146	184 ValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeu 203	GluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArg SerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeuAspTyrGlu	965 GCCCGGCTGTGCGAGGCGACACTGAGTGCCGGGAGTACTGGCCA 1009 324 SerAlaGlyGluHisAsnProPheLySGlyAlaIleAsnPheAspAsnIleGlyTyrAla 343 1010GGACCCAACTTTGGCATCACCAACTTTGACAATATCCTGTTTGCC 1054 344 TrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheVal 363 ::: ::	383 SerPhePheMetileAsnLeuCysLeuValValileAlaThrGlnPheSerGluThrLys 402
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1465 1465 -- 1435 3GTTTGCAGAT---- 1465 1465 1465 1570 ATTACAACCAGCCGCGCGCTTACCACGACCCTGTAT 1690 /sasnProTyrasnIlePheAspGlyValIleValVal 816 -------AAGGAGAAGATGTTCCGGTTT 1564 lyGln------GlnGlyGlyLeuSer 831 GGGGGCCATCAAGCCGGGAAGCTCCTTTGGGATCAGT 1870 1564 ||||||| stctcttcctcacagagatgtccctgaagatgtatggc 1750 isTyrHisLeuGlyAsnGlyThrLeuArgAlaProArg 516 rgAspAlaAsnGlySerArgArgLeuMetLeuProPro 536 lyAlaProProGlyGlyAlaGluSerValHisSerPhe 556 luProValArgCysGlnAlaProProProArgSerPro 576 1GlySerGlyLysValTyrProThrValHisThrSer 596 luLysAlaLeuValGluValAlaAlaSerSerGlyPro 616 969 ppLeuArgAspProHisSerArgArgGlnArgSerLeu 716 srleupheAlaLeuGluMetLeuLeuLysLeuLeuVal 796 ysGlnSerSerCysLysIleSerSerProCysLeuLys 656 rValLeuAlaPheTrpArgLeuIleCysAspThrPhe 736 rHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 776 leProProGlyProTyrSerSerMetHisLysLeuLeu 636 rgSerHisArgArgLeuSerValHisHisLeuValHis roAspSerCysProTyrCysAlaArgAlaGlyAlaGly luMet ProAspSerAspSerGluAlaValTyrGluPhe ------TTTATC DAGAGGTCGTCATACTTCCGGAGG------

	1349 LeuaspGlyLeuLeuvalLeulleServallle 1349 LeuaspGlyLeuLeuvalLeulleServallle 1368 AspSerGlyThrLysIleLeuGlyMetLeuarg 1368 AspSerGlyThrLysIleLeuGlyMetLeuarg 1368 ProLeuargVallleSerargAlaGlnGlyLeu 1388 ProLeuargVallleSerArgAlaGlnGlyLeu 1388 ProLeuargVallleSerArgAlaGlnGlyLeu 1388 ProLeuargVallleSerArgAlaGlnGlyLeu 1408 SerLeulySProlleGlyAsnileValVallle 1408 SerLeulySProlleGlyAsnileValVallle
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rgValLeuArgLeuLeuArgThrLeuArg 1387 :: ||||||| aGTCTCTGAGAGTCCTTCGTGTCCTGCGG 3916 lnalaTyrLeuArgSerSerTrpAsnVal 1348
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sagccratTrccgGGACTTGTGGAACATT 3808 leAspileLeuValSerMetVal---Ser 1367 |||||||::: 3rGGCGCCCTGGTGGCTTTGCTTTCTCA 3856 eulysLeuvalValGluThrLeuMetSer 1407 |||||| rcaaggcrgrtrrgacrgrgrgaac 3976 leCysCysAlaPhePheIleIlePheGly 1427
:: neProProGlnSerArgPheArgLeuLeu 1268 spHisValValLeuVallleIlePheLeu 1288 :: |||:::|||||||| \GGTGGTCATTCTCGTGTCATCGCCTTG 3631 CCCAGTGATGCTGACGGCCCTTTTGG 3412 sileAspProHisSerAlaGluArgile 1308 3352 ----SerLysGlyGluArg 1235 CCTGGAAAGCCAAGCAGAGGAAAA 3472 ::: --GTGCGCACAGACTCGCCCAGGAACAAC 3688 GGCCCGGCACAAGCCGCAGCCTGCTCAC 3112 uGluSerSerGluGluGluGluArgAlaSer 1152 | ::: ::||| |GCCACGGAGAAGGAGGCTGAGATAGTG 3172 rLeuGluArgGluAlaLysSerSerPhe 1172 ccagcccccddddccacacrcrgaccrg 3232 uHisArgThrAlaSerGlyArgGlySer 1192 :||| |GCACACACTGCCCAGCACCTGTCTCCAG 3292 rAlaSerGlyArgLeuAlaArgAlaLeu 1212 plleargalaargLeuProAlaCysTyr 1248 CCAGGATCCGAGCAAGGAGTGCGCCGGC 2992 CGGCCCCCGAGCGGGCCCCGGGAGGCG 3052 ----TCAGCGGAACGTCACTCGCATGGGCAGT

784CCTGTG	; ORGANISM: Rattus norvegicus ; FEATURE:
284 SerValProThrLeuArgGlyAspGlyG	LENGTH: 7011 TYPE: DNA
783	SOFTWARE: FastSE SEQ ID NO 9
264 GluAspGluSerProPheIleCysSerG	PRIOR FILING DATE: 1998-03-13 NUMBER OF SEQ ID NOS: 28
763	PRIOR FILING DATE: 1999-03-12 PRIOR APPLICATION NUMBER: US 60/077,901
244 ProGluAsnPheSerLeuProLeuSerV	PRIOR FILING DATE: PRIOR APPLICATION
706 ATGTTCGCTATCATCGGCCTCGAGTTCT	CURRENT PRIOR A
224 IlePheGlyIleValGlyValGlnLeuT	FILE REFERENCE: BL
46	anie N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
9	FUBLICATION NO. USZUDOJISS/SIAI GENERAL INFORMATION:
86 GTGCTTAGG	Sequence 9, Application US/11350336
184 ValleuArgProLeuArgAlalleAsnA	RESULT 6 113-11-350-336-9 Ox
ACAGCTGGAACTGA	رر ووءو در ووءو
	Qy 2224 AlaProSerSepSerLysAspPro 2232
481 TACCTCCGGAATGCCTGGAACGTCATGG	GCAGCCACCCAACGTCG
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128 PheAlaValGluMetValValLySMetV	Qy 2197 ProProSerIleThrIleAspProProGluSerGln
361 GGGGACAAGACTCCCCATGTCTGAACGAC	GCCGGTCCCAGGAGCGGAGGCAGC 649
	GlyGlyProGlySerArgProLysLysLysLeuSer 2196
313 ATCATCGCCAACTGTATTGTCCTGGCCC	creccecedadadacta-cae 6434
61	Qy 2157 HisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspPro 2176
	Db 6370 6393 Db 6370 6393 Db
	luGlnArgArg 2156
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133 TACAAGCAGTCCATTGCGCAACGCGCAC	2118 LeuproProGlyGlyGlnGluGluProProSerProArgAspLeuLysLysCysTyr 2136
47 GluAlaGluGlyLeuProTyrProAlaLe ::: ::	OY 2098 Programmargserserrenginteruneuseintpiresersiyaspie 211, 0y
73 GGGGCGGCGGGCCGGTGGCCCGGGCCA	CACCACCA 63
27	Qy 2081 ThrProProAlaProGysProGlyProGluProAsnTrpGlyLysGlyPro 2097
1-257A-37 (1-2266) x US-11-350-	Db 6212TCCACGCTGGCCCAGCGGCCCCGTGGGAC-TCATCTTTGCAGCACCACCC 6261 US
cch: 14.5% 8	1nHisSerArgSerHisSerLysIleSerLysHisMet 2080
	DD 6164 GCCGAGACTCAGCCGTCACAGCCCCATGAAGCGCTCCATC 6211 Be
1.81e-68 1728.50	aTyrSerPheTrpGly 2060
SOOK	Db 6104 GGGGAGCCCCAGCCTGGACCAGCCAGCCAGCCAGCCACCCTCCATGCCCCGCCTTGCG 6163
LOCATION: 17008	Qy 2027ThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAla 2043

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||| |----GTGACTTTCCTTGTGGCAAGGAGCCCCT 819
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GAGATCGGGCTGCTGCTTCTTCGCCATCCTC 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValalaLeuGly---IlePheGlyLysLysCys 146
:::|||||||||
ATAGCTCTGGGCTTCGTGTTCCACAAAGGCTCC 480
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                                                                                                                                                                                                                                                                                     252
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                                                                                                                                                             CAGGGGGTCTGCCGCCGGCCAGCGGGTCCTG 132
                                                                                                                                                                                                               CGGACCATGGCCCTGTACAACCCCCATCCCAGTC 192
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                                                                                                                                   SerAlaGluLysAspProglySerAlaAspSer 46
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rggaattccaagcttgcaggtggtgctcaagtcc
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TATATGGGCAAATTCCATAAGGCCTGCTTC---
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|------ACCCTGAGGGCTGTGCGT
                                                                                                                                                                                                                                                                        AsnValSerPheSerAlaValArgThrValArg
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CTG------GAGCAGCACCTCCCTGAT
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È	304 AlaTyrAsnSerSerSerAsnThrCysValAsnTrpAsnGlnTyrTyrThrAsnCys 323		
qa	ω !	Dp	1387
ò	324 SerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnileGlyTyrAla 343	ζζ	676 GlyGluValGluLeuAlaAspArgGluM
QQ	865GGACCCAACTTTGGCATCACAATTTTGACAACATCTTGCC 909	<u>අ</u>	
ò	344 TrpileAlailePheGlnValileThrLeuGluGlyTrpValAspileMetTyrPheVal 363	ò i	<pre>6 PheThrGlnAspAlaGln 6 </pre>
qa	910 ATCTTGACCGTGTTCCAGTGTATCACCATGGAGGGCTGGACTGACATCCTCTACAATACA 969	g 3	LAC-1
ò	364 MetAspAlaHisSerPheTyrAsnPhelleTyrPhelleLeuLeullelleValGly 382	ò t	716 LeuGlyProAspAlaGluProSerSerVe
qq	970 AATGAGGGCGGCAACACGTGGAACTGGTTGTACTTCATCCCCCTCATCATGGC 1029	<u> </u>	m (
λ	383 SerPhePheMetlleAsnLeuCysLeuValVallleAlaThrGlnPheSerGluThrLys 402	è 16	/36 PheArgLyslleValAspSerLysTyrPP
qa	1030 TCCTTCATGCTCAACCTGGTGTTCGTGTTTCAGGAGGTTTGCCCAAAGAGCGG 1089	ସମ <i>.</i>	، و
ò	403 GlnArgGluSerGlnLeuMetArgGluGlnArgValArgPhe 416	∂ <i>t</i>	756 AsnThrLeuSerMetGlyIleGluTyrHi
qa	1090 GAGCGAGAACCGCCGTGCCTTCCTGAAGCTCCGCAGCAGCAGAATTGAG 1146	g ;	1486 AACACGTTGTGTGTGCCCATGGTACACTY
ò	417 LeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeu 436	Š å	
qa	1147CGAGAACTG 1155	g ::	
ò	437 LeuLysTyrLeuValTyrileLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArg 456	ò i	
QΩ	1156 AATGGGTACTTGGAGTGGATCTTCAAGGCGGAGGAAGTCATGTTGGCAGAGGACAAG 1215	0 0	
δ	457 AlaAjaGlyValArgValGlyLeuJeuSerSerProAlaProLeuGlyGlyGlnGluThr 476	δλ	816 ValileSerValTrpGluileValGlyGl
qq	 1216 AACGCAGAAGAGAAG 1230	ବ୍ର	1666 GTGGGGAGTATCTTTGAAGTAGTCTGGG
ò	49	δλ	831 SerValLeuArgThrPheArgLeuMetAr
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qα		qa	
δ	516 ArgAlaSerProGlulleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuPro 535	ò	871 LeuLeuMetLeuPhellePhellePheSe
QQ	::: :::	qq	
ò	536 ProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSer 555	ò 1	891 PheAlaSerGluArgAspGlyAspThrLe
qa	1314 1314	Q D	9
Qy	556 PheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSer 575	δ	911 TrpAlaIleValThrValPheGlnIleLe
qq	1314 1314	ad j	
ò	576 ProserGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThr 595	λο ·	_
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δλ	596 SerProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGly 615	λ i	94
qa	1315	aa ·	ď
ò	616 ProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeu 635	ð 7	966 GlyPheGlnAlaGluGluIleSerLy
qq	1342 CCCTTTGCTCGTGCCAGCCTC1362	an '	d+ ,
Š	636 LeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeu 655	ð :	81
qa	1363AAGAGTGGGAAGACAGAGACTCA	gg ,	94
δλ	656 LysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAla 675	λδ 	986 GlnLeuProValAspSerGlnGlyGlyAs

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on o	138/	
δ	919	ArgGluMetProAspSerAspSerGluAlaValT
Db	1402	AAGGAGAAGATGTT
٥٧	969	rAspLeuArgAspPr
Ор	1420	TTC
ò	716	LeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThr 735
QQ	1423	
δ	736	uVa
qq	1426	CCTG 14
οχ	756	AsnThrLeuSerMetGly1leGluTyrHisGluGluGluGluGluLeuThrAsnAlaLeu 775
qq	1486	
٥٧	176	GluileSerAsnileValPheThrSerLeuPheAlaLeuGluMetLeuLeuLygLeuLeu 795
o qu	1546	AC 16
δλ	796	ValTyrGlyProPheGlyTyrlleLysAsnProTyrAsnIlePheAspGlyValIleVal 815
QQ	1606	CTAGGGCCCAGAAGCTACCGGTCTTCCTTCAACTGCTTTGACTTTGGGGTGAT
Qy	816	yGlyGlyLe
pp	1666	CAAGCCAGGAACCTO
δγ	831	SerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAla 850
qa	1726	AGTGTGCTGCGGGCTCTCCGACTGTGGGATTTTCAAAGTCACCAAGTATTGGAACTCC 1785
Qy	851	LeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMet 870
qq	1786	CTGAGGAACCTGGTTGTTTCCCTCCTCATCATGAAGTCCATCATCATCTTCTTC 1845
Qy	871	LeuLeuMetLeuPhellePhellePheSerIleLeuGlyMetHisLeuPheGlyCysLys 890
qq	1846	crecitricatreserciticercretreses 1905
δλ	891	Serbeubeu 910
qq	1906	TTCAACTTTCAAGATGAGACTCCAACCACCAATTTTGATACCTTCCCA 1953
٥٧	911	<pre>TrpAlalleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyr 930 ::: </pre>
qa	1954	gcreccarccrcacteratricagaricitateagagagagagagagagagagagagagagara 2013
0y	931	AsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIle 945
qq	2014	20
٥٨	946	AlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGlu 965
DD	2074	C 21
٥y	996	GlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
qq	2134	AACCTTGCCAATGCCCAGGAGTTGACCAAGGATGAAGAGGAGATGGAAGAGGCAGCCAAT 2193
٥'n	981	
qq	2194	CAAAGAAGTAGCTGAAGTCAGCCCCATGTCT
٥y	986	GlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPhe 1005

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1006 F 2314 C	PheserProserLeuaspoiyaspoiyaspangsbysbysboundatedvangtron - 22 :::	셤 :
	GlyGluHisProGluLeuArg 1032	දුරු අධ
2374 P	ATGGACCCGGAGGAGCGCCTGCGTTATGCCAGCACGCCCACGTGAGGCCAGGACATGAAG 2433	ô
1033 I	LysSerLeuLeuProProLeuIleIleHis	. අ <u>අ</u>
2434 7	249	δλ
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2554 (CACCACCGGCATCGTGATAGGGACAAGACCTCAGCCTCAACCCCTGGTGGAGGCGAACAG 2613	ò
1048	MetSerLeuProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAla 1065	. 원
2614 (λō
	SerArgArgThrSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysSer 1085	qa
2674 (CGCCCTCGTCGAAGTCACAGCAAGGAGGCTCCAGGGGCTGACACACAAGTGCGTTGT 2730	٥٨
1086	0	qa
2731 (GAGCGCÁGTAGACGTCACCACCGGCGCGCGGATCCCCGGAGGAGGCCACTGAACGGGAACCT 2790	ò
	ArgargSerSerArgAsnSerLeuGlyArg 1115	qa
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1211	AlaLeuArgProAspAspProProLeuAspGlyAspAspAlaA 1225	qa —
3196	GGCAGTC	ò
1225	spaspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrp 1239	qa
3256		ò
1240	IleArgAlaArgLeuProAlaCysTyrLeuGluArgAspS 125	qa
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	499CCAGAAGACTCTGGACTTACTGGTGCCACCCCACAAACCTG 553	1949AlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGl 1964 	1964 nSerGlySerValLeuSer-ValHisSerGlnProAlaAspThrSerTyrIleLeuGlnL 1984 : ::	1984 euProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleP 2004	2004 roLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgA 2021	2021 rgGlnAlaAlaIleArgThrAspSerLeuAspValGln	2036 lySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAla- 2055 5825 AGAGGACCCAGGACGTACTTTATGAGGCCAGAGCACCTCTAGAACGTGGCCATTCTGCAG 5884	2056 TyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArg 2071	2071 2071 5930 TGCAGAACATGAGAGGACCGGATGGGGAGCCCCAGCCTGGCGTGGAGAGCCAAG 5989	2072ProAla 2084 2072	085 ProCysProGlyProGluProAsnTrp	2093 2093 2093	2094GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThr 2108 :::	2109 GluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlyGluGluBro 2126	2127 ProSerProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArg 2146	2147 ProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSer 2166 :: :: 6340 CCCTCCTCTTTTCAGAGAAGCAGCGCTTCTATTCCTGTGACCGCTTT 6390	2167 GlySer 2176 ClySer 2176 ClySer	2177
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1594 yrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluH 1614 :::	1614 isTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrV 1634	alilePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePheG 165	InAspArgTrpAsnGlnLeuAspLeuAlaileValLeuLeuSerileMetGlyileThrL 167 ::	euGluGluIleGluValAsnAlaSerLeuProlleAsnProThrIleIleArgIleMetA 169 ::	rgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaL 171	euLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetL 173	euLeuPhePhellePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspG 175::: ::::	1754 luThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaP 1774 ::	heLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrL 179 :::	euArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleS 180 	erProlleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValI::::::: :::::: ::::: ::::	1829 leAlaValLeuMetL 1834 :: :: 5111 TTGCTGATCATCACACAATTTCCAATACCTCCCCCCAATTCTAACCCCCC	ysHisLeuGluGlu-SerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeu 185	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySer 187	ProPheLeuTrpPro-GlyValGluGlyProAspSerProAspSerProLysProGlyAl 189	191		5387 TGGCCCTCATCCGGACGCACTGGAGATCAAGCTTGCCCCAGCGGGACAAAACAGCACC 5446 1920 oAspLeuLeuThrValArgLysSerGlyValSerAr 1932
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180 CTCCAAAAAGCTGCCAGATCTATGGCAATCCACCCCAAGAGCTCATGGAGAGCCCT 239 93 PPYCALALEUALAPPOVALVAIPHEPHETYLEUSERGINASDSER	1 roalArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuVa 2	Oy 283 gSerValProThrLeuArgGlyAspGlyGlyGlyGlyGlyProProCysGlyLeuAspTyrGl 303 283 gSerValProThrLeuArgGlyAspGlyGlyGlyGlyGlyProProCysGlyLeuAspTyrGl 303 Oy 283 gSerValProThrLeuArgGlyAspGlyGlyGlyGlyGlyProProCysGlyLeuAspTyrGl 303 Oy 303 uAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCy 323
6451 GCGGCACTAGAG 2185 2185 6511 ATGTCAACATCT 6511 ATGTCAACATCT 2194 LysLeuSerPrc 2194 LysLeuSerPrc 2208GlnGlyPrc 2208GlnGlyPrc 2218IleCy 6631 GCTGAGGGTCAG 6631 GCTGAGGGTCAT 6631 GCTGAGGGTCAT 6631 GCTGAGGGTCAT 6631 GCTGAGGTCCC 2218IleCy 2218IleCy 6691 GAACACACTGC 2245 ProSerProLy 3258 SerSer 2259 6862 TCCTCC 6867 5811-313-450-9 Sequence 9, Application	obeologe deorge deorge High-J Selec NUMBER: 2001-11 UMBER: 2000-11 S: 41 or Wind	Alignment Scores: 2.78e-66 Length: 6051 1678.00 Marches: 590 2.08e-10 Marches: 377 42.3\$ Mismatches: 378 14.1\$ Mismatches: 530 16.1\$ Mismatches: 530 16.1\$ Mismatches: 83 17.2\$ Mismatches: 83 18.1\$ Mismatches: 83 19.1\$ Mismatches: 83 10.1\$ Mismatches: 83 11.2\$ Mismatches: 83 12.0\$ GGAGGCGGAGGAGAGGGGGAGAAGCCCCGGGCCCAGCTGGAGCTGCAGGCTGCAGGCTGCAGGCTGCCGGGCCCCGGCCCCGGCCCAGGAGGGCTGCCCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCC

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qa	329	λŏ	1490
λ	16	qa	4267
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qa		ò	1530
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٥٧	24	qa	4507
qq	352	δλ	1588
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δ	20	qa	4627
qq	363	λŏ	1627
δ	30	qa	4687
qq	369	λŏ	1647
ò	32	qa	4744
qa	375	δλ	1667
ζ	LeuGlyTrpCysPheGlyGluGlnAlaTyr 134 ::: :::	qa	4801
q	TGCTCAAGTGGGTGGCCTACGGCTTCAAGAAGTAC 379	δ	1687
δδ	LeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIle 136	qa	4855
qa	TTCACCAATGCCTGGTGCTGGCTCGACTTCCTCATCGTAGACGTCTCT 384	٥٨	1707
λ ₀	1362 LeuValSerMetValSerAspSerG1yThrLyslleLeuG1yMetLeuArgValLeu 1300	_	

ValThrMetAlaMetGlu----HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLys 1626 LeuSerileMetGly1leThrLeuGluGluIleGluValAsnAlaSerLeuProlleAsn 1686 4626 AsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGlu 1549 1607 :::::: caggacatcttcatgacagaggagcagaagaagtactacaatgccatgaagaagctgggc 4506 ArglysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHis 1587 1469 4206 1489 valvalGluThrLeuMetSerSerLeuLysProlleGlyAsnIleValValIleCysCys 1420 ijeCysAsnTyrIlePheThrValijePheValLeuGjuSerValPheLysLeuValAja HisLeuCysThrSerHisTyrLeuAspLeuPhelleThrGlyValIleGlyLeuAsnVal PheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeu 7 TCCAAGAAGCCCCAGAAGCCCATCCCACGGCCCTGAACAAGTACCAGGGCTTCATATTC AspileMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHis GluGluAlaArgArgArgGluGlu-----LysArgLeuArgArgLeuGluLysLysArg AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal AspCysAlaGluAlaSerTyrArg------TrpValArgHisLysTyrAsnPhe ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu AspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpVal |||||||:::||| | GACAACGTGGGGGCCGGGTACCTGGCCCTTCTGCAGGTGGCAACATTTAAAGGCTGGATG --AsnLysSer CAGTGTGAGGTCCTTGACTGACCGGAGAATTGTACTGGACCAAGGTGAAAGTCAACTTT Cys-----GlnGlyGluAspThrArgAsnIleThr----

190 IGLINRET VALUE ALLE VALUE ALA
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 3238ATTGCACCTGGGGAATCCGAT	1148 luGluArgAlaSerProAlaGlySerAspHisArgHisArg ::: ::: :::::: 3278 AGGAACTTAGCAGTGATTCGGATAGTGAATAC	laLysSerSer		1188 erGlyArgGlySerAlaSerGluHisGlnAspCysAsnGly	1208 euAlaArgAlaLeuArgProAspAspProProLeuAspGly	3352ACAGTTGATAACCCTTTGCCTGG	1228 lyAsnLeuSerLysGlyGluArgValArgAlaTrpIleArg	3395 CTGAACCTATGAATTCCGATGAGCCAGAGGCCTGTTTCAC	3455 TCTCATGCCAAGTTAACATAGAGTCAGGGAAAA	1264 rgPheArgLeuLeuCysHisArgIleIleThrHisLysMet	3506 ACATCAGGAAAACCTGCTACAAGATTGTTGAACACAGTTGG	1284 alileilePheLeuAsnCysileThrileAlaMetGluArg		3626 AGACCATTAAGATTATCCTGGAGTATGCAGACAAGATTCTC	1324 luMetThrValLysValValAlaLeuGlyTrpCysPheGly	3686 AAATGCTTCTAAAATGGATAGCATATGGT	1344 erSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSer		1364 ermetValSerAspserGlyThrLyslleLeuGlymetLeu 			1404 hrLeuMetSerSerLeuLysProlleGlyAsnIleValVal			TGA	1442GinglygiuAspiniagashileiniash 		TTATGAA	1473 lyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAsp(
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rgGlySerLeuGluArgGluA 1168 lyAspAspAlaAspAspGluG 1228 |||::: AAATCTGG-----TGGA 3505 roGlyLeuHisArgThrAlaS 1188 lyLysSerAlaSerGlyArgL 1208 rg------1244 YrijePheProProGlnSerA 1264 et phe AspHisValValLeuV 1284 ||||::: \ATATTTATTGAAAGGAAAA 3625 neThrAlaValPheLeuAlaG 1324 |||||| :::|||::: | rcacttacatcttcattctgg 3685 rValileAspileLeuValS 1364 -----AGCAAAGTGAGAT 3322 ||::: 3AGAAGGAGAAGAAGCAGAGG 3394 CAGATGGTTGTGTACGGAGGT 3454 gProLysileAspProHiss 1304 yGluGlnAlaTyrLeuArgS 1344 || ::: |||| STTATAAACATATTTCACCA 3733 ||:::::: CTTTGGTTACTTTAGTGGCAA 3793 uArgValLeuArgLeuLeuA 1384 :::: |||||||| TAAATCCCTTCGGACACTGA 3844 |yLeuLysLeuValValGluT 1404 ||::::::::|||||| |sAaTGAGGGTCGTTGTGAATG 3904 allleCysCysAlaPhePheI 1424 sphePheValCys---- 1441 ||||::: ||| GTTCTATGAGTGTATTAACA 4024 nLysSerAspCys---- 1455 |:::|||:::||| |TCGTTCCGAATGTTTTGCCC 4084 pGlyTrpValAspIleMetT 1493

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                                             etLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheV 1533
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Sequence 8, Application US/11251465

Publication No. US20060094061A1

GENERAL INFORMATION:

APPLICANT: Brys, Reginald

APPLICANT: Vandeghinste, Nick

APPLICANT: Tomme, Peter

APPLICANT: Klaassen, Hubertus

TITLE OF INVENTION: Molecular Targets And Compounds, And I

TITLE OF INVENTION: Inflammatory Diseases

CURRENT APPLICATION NUMBER: 60/619,384

PRIOR APPLICATION NUMBER: 60/619,384

PRIOR PELING DATE: 2004-10-15

NUMBER OF SEQ ID NOS: 880

SOFTWARE: PatentIn version 3.3

SEQ ID NO 8

LENGTH: 6371

TYPE: DNA

ORGANISM: Homo sapiens

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	31	::: ::: 3 TGTATATTTATTTGCGTCTTTATCATCTTTGGGTCATTCTTCACTTGAACTTGTTCA 437	

1838 1877 alGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisA 1897 ::: |||||||::: |||||| | 5367 1771 1791 5128 4963 4729 4843 1751 1591 1631 1651 luSerAsnLysGluAlaLysGluGlu---AlaGluLeuGluAlaGluLeuGluLeuGluM luCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheG CACCTATTĊTTAACAGTAAGCCACCCĠĂĊTĠŦĠĀĊCCAAAAAAAGTTCATCCTGGAAGTT euThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLySHisLeuGluG ::: ::|||::: ||| TTGCCACTGAAGAAGTACTGAACCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAG- $\verb"ethysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyV"$ ------GTTTGGGAGAGT et ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuL :::|||::: ------GATGGAATTAATGACATGTTCAATTTTGAGACCTTTG laMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrI lepheThrValIlepheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgA ::|||||||::::::::||||||||:::::: TTGGTGTCATCATAGATAATTTCAACCAACAGAAAAGAAGGCTTGGAGGTCAAGACATCT --LysArgLeuArgArgLeuGluLysLysArgArgLysAlaG TTATGACAGAAGAAGAAATACTATAATGCAATGAAAAAGCTGGGGTCCAAGAAGC lnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysT hrSerHisTyrLeuAspLeuPhelleThrGlyValIleGlyLeuAsnValValThrMetA lylleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleA CACAAAAGCCAATTCCTCGACCAGGGAACAAATCCAAGGATGTATTTTGACCTAGTGA ysAspThrLeuArg-----AspCysAspGln----AAAAGGAA---rgArgArgGluGlu 5189 1838 1818 5249 5024 1751 4673 1651 1671 4790 1691 4844 1711 4904 1731 4964 1771 1791 1611 4493 1591 4373 S S S δ

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qa	GAGAAGCAGCAGCAGCAGGAGGATCTAAAAGGCTA 14	δ	789 luMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrlleLysAsnProTyrAsnI 809
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qq	CTTGGATTGGATC	ζō	valileSerValTrpGluI 822
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Qy	<pre>593 alHisThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaS 613 ::: </pre>	qa	.: 49 caggaatgatcgtctacatctacttcatcctcttcatttgtatatt
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qa	3351	TITICATCCICIACAAGGAIGGGGAIGTIGACAGICCIGIGGICCGIGAACGGAICIGGC 3410
٥٨	1463	alArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuA 1483
qa	3411	AAAACAGTGATTTCAACTTCGACAACGTCCTCTGCTATGATGGCGCTCTTCACAGTCT 3470
δδ	1483	laSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspG 1503
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                        ON: Transcriptome Microarray Technology and ON: Methods of Using the Same 55815-0102 (319189)
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NATE: 2005-11-03
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GENERAL INFORMATION:
APPLICANT: Harkin, F
APPLICANT: Johnston
APPLICANT: Mulligar
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FILE REFERENCE: 5881
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GlyProSerProP

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CURRENT APPLICATION NUMBER: US/11/313,450
CURRENT FILING DATE: 2005-12-19
PRIOR APPLICATION NUMBER: 09/989797
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-22
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à	Φ.	rCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyBlyProProCysGl	
ą	933	TTTCTACACAGTTCCTGGCATGCTGGAACCTTTACTCTGTGG	974
<i>\</i> 2	299	yLeuAspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTy 	319
q	975	GGAGGGATACTGATGCTGGGCAATGCCCAGAGGGATACCAG	101
<i>≿</i> ;	319	rTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAs	339
ą	1015	TGTATGAAAGCAGGAAGGAACCCCAACTATGGTTACACAAGTTTTGACAC	1064
<i>\</i> 2	339	nileGlyTyrAlaTrplleAlailePheGlnValileThrLeuGluGlyTrpValAspil	359
ą	1065	TTTTAGCTGGGCCTTCTTGGCATTAŤŤTCGCCTTATGACCCAGGACTATŤGGGAAAACTT	
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ą	1365	::: AGGAACTGTCTCAGAAGATGCCATAGAG	1392
ζ	449		469
ą	1393		1418
≿	469		489
ą	1419	: CCTTCGGAGCTCTTCTGAAATCTCTAAACTCCAAAGAGTGCAAAGGGAAAGACGT	1476
≿	489		509
ą	1476		1476
λ;	509		529
ą	1477		1532
λį	529		548
ą	1533		1592
≿ i	549		563
ą	1593		1646
≿ :	563	euGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSerG	581
ą	1647		1706
λį	581	lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluT	601
ą	1707		1751

ò	601 hrLeuLysgluLysglaLeuValGluValAjaAlaSerSerGjyProproThrLeuThrS 621	ŧ	0
qa	1752 GGATGACGACGCACGGTGGAGGAGAGGGCCGCCGCCGGGGACTCCCTCT 1804	3 8	0 0 0
δ	621 erLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSerT 641	Z qq	282
ą	1805TCATCCCCATCCGGGCCCGCAGCGCCGGAGCAGCTA 1841	۶ ک	94
ò	641 hrGlyAlaCysGlnSerCysLysIleSerSerProCysLeuLysAlaAspSerGlyA 661	G QQ	288
qa	1842 CAGCGGCTACAGCGGCTACAGCCAGGCGCTCCTCGCGCATCTTCCCCAG 1895	ò	96
λΌ	661 laCysGlyPro	- ਰ ਹ	294
qq	CGTGAAGCGCAACAGCACG	ò	98
δ	673 laGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla- 692	점	300
QQ	1956 cegcedecececerce-cacarcegedecerecereceagegearacaacreaderes 2014	ò	100
λ		연	301
qa		δ	102
ò	SerAspleuArgAspProH	qa	305
Ωp	GGCGGAAGGACAGAATCAACAGTATAATGAGTGTTGTTACAAATACACTAGTAGAAGAAC	δδ	104
ò		qa	311
qq		٥y	105
λŏ	SerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheA 737	QΩ	316
qq		ò	107
ò	737 rgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnT 757	qq	320
ф	2240 ACTIGATAGTTATGGACCCTTTTGTGGATTTAGCCATCACCATCTGCATCGTCCTGAATA 2299	λ	109
ò	777	qa	320
q		δy	111
ò	777 leSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValT 797 :: :::	Ωp	326
qa		ò	113
ò	797 yrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValI 817	qa	330
qg		Ø	115
δ	37	qq	336
q		Qy	117
ογ	57	q	341
qa		ò	119
δ	857 alLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPhelleP 877 ::::: :::: : ::: ::::	q	344
qq	2600 TTATTGGAAATTCAGTGGGTGCCCTGGGCAACCTGACACTGGTGCTGGTGCTTATTGTCT 2659	ò	121
δ	hellepheSerlleLeuGlyMetHisLeuPheGly	qo	344
qq	ITGGTGGGGATGCAACTCTTTGGAAAAAGCTACAAAGAGTGTGTCTGCA	ò	123
ò	ysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuL 	qu	35(
da	AGATCAACCAGGACTGTGAACTCCCTCGCTGGCATATGCATGTTTT	δλ	124
λο	910 euTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuT 930	_	

ρ	2768 TC	TCCATTCCTTCTTTTTCGAGTGTTGTGCGGGGAGTGGATTGAGACCATGT 2824
. ;		
<u>م</u> ج		ACTGCATGGAAGTGGCCAGGCCATGTGCCTCATTGTCTTTTATGATGGTCATGG 28
>	949 hr	hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 969
q	2885 TG	arregeaacrregregregregacrefactrarregecrregecrecrregre 2944
Á	696	laGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProV 989
ą	2945 CA	300
λ;	989	InglyglyAspAlaAsnLysSerGluSerGluProAspPhePheSerProS 100
q و	3002 TG	300
λ;	σ.	lyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHis- 102
ą و	3010	700
≿	O.	
ಧ	3050 CC	310
<i></i> }⁄	1042	05
ą	3110 TG	316
λ	1058 Le	Ser(
ą	3167 AT	ATGGCACAACCA 320
<i>≿</i> ;	1078 Gl	GlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrp 1097
qc	3203 GC	GCGGCA3208
λ.	1098 Se	erAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArg 1115
q(3209	-TTGGCAGCAGCGTGGAGAAGTACATCATT-GATGAGGACCACATGTCCTTCATCAAC 3264
λζ	1116 Al	AlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu 1135
qc	3265 AA	ccccaactigacigiadgegacccariectergegegegegegegegegegegegegegegegegegeg
λ	1136 Gl	GlyGlnGluSerGlnAspGluGluGluSerSerGluGluGluArgAlaSerProAla 1154
qo	3307 TC	TGACTTTGAGAACCTCAACACAGAGGATGTTAGCAGCGAGTCGGATCCTGAA 3360
λά	1155 Gl	_
qq	3361 GG	341
λά	1175	ProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAla 1193
g G	3418 AA	1
δλ	1194 Se	sSerAlaSerGlyArgLeuAlaArgAla
qq	3442	GTGGAA 3447
δý	1214 Pr	122
qq	3448 CP	350
ò	1229	
qa	3508 AZ	AAGTGCTGCCAGGTCAACATCGAGGAAGGGCTAGGCAAGTCTTGGTGGATC3558
٥y	1244 Le	LeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePheProProGlnSer 1263

Application Application		ò -	1610 MetAlaMet(
10.00000000000000000000000000000000000	4 ArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeu 128	qa	. LO
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### ADDRICKTOCKCATCCTGGAATNATCTGLAAATTCTCCCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTTCACCTATAATCTCACCTACAATCTCACCTATAATCTCACCTATAATCTCACCTATAATCTCACCTATAATCTCACAATCTCACAATCACAATCAAATCTCACCTACAATCAAATCTCACCAATCAAATCTCACAATCAAATCTCACAATCAAATCTCACAATCAAATCTCACAATCAAATCTCACAATCAAATCTCACAATCAAATCAAATCAAATCTCACAATCAAAATCAAATCTCACAATCAAAATCAAATCAAATCTCACAAATCAAAATCAAATCTCACAAATCAAAATCAAAATCAAAATCAAATCAAAATCAAATCAAATCAAAATCAAATCAAAATCAAATCAAAATCAAATCAAAAATCAAAATCAAAATCAAAAATCAAAAATCAAAAATCAAAATCAAAAATCAAAAATCAAAAAA	SerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAla 132	δ	0
	AAGACCATCGGCACCATCCTGGAATATGCTGACAAAGTCTTCACCTATATCTTCATCATC 373	යු <u>ට</u>	29
GaidatigntsGatCadcaccccCcartacccccccccccccccccccccccccccc	GluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArg 134	<u>ک</u> ظ	1669 IleMetGly:
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SerMetValGeTGGACTGATCCATCATATGGCTGCTCTTTAGGT 3843 SerMetValGeTGGACTGGACTCCATTGAGGCTGCTCTTTAGGT 3843 WATCCCTGGAGGCGCTGAACTCCATTGAGGCTGCTCTTAGGT 3844 WATCCCTGGTGGCGCCTTTAGGGGTGCCGTGAAACTCCTTAGGT 3894 WATCCCTGGTGGCGGCCTTTAGGGGTGGTGGTGAACTGTGGTGAACTGAGGTGGTGAACTGAGGTGGTGAACTGAGGGTGGTGAACTGTGAGGGTGGTGAACTGTGGTGGGTG	SerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuVal 136	දු අය) 44) (U
SerMecValSerSapperGy/Throys:lelendly/MetLeukrgferleuk 1383 ANGTOCKTO	AATGCCTGGTGTTGGCTGGACTTCCTCATTGTGGCTGTCTCTTTAGTCAGCCTTATAGCT 384	ζ	O.
######################################	SerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeu 138 ::: :: AATGCCCTGGGCTACTCGGAACTAGGTGCCATAAAGTCCTTAGGACCCTA	qa	4903 AAAGGGATTC
### AGACTTYCRAGATCCTATACACCATACACCATACACCACATACACCACATACACCATACACCATACACCCTACACCATACACCCTACACCAC	4 ArgThrLeuArgProLeuArgVallleSerArgAlaGlnGlyLeuLysLeuValValGlu 140	δ	1729 GlyLeuLeuf
ThrieuwetserSerLeuLysProlleclyAsnileValValileCysCysAlaPhePhe 1423 GCCTTGGGGGGCCCTCCCTCGTGGGGGGGGGGGGGGG		qu	
	1 ThrLeuMetSerSerLeuLysProlleGlyAsnileValValIleCysCysAlaPhePhe 142	δ	1749 AspLeuGluC
	::: ::::::	qa	
CTGATTTTCAGCATCATGGGGGTAACTTCTTTAAT 4074 G1UABPTHAYGABILETHABILYSSERASDCYSALGGI134 GAGCTTCTGAAATTCGAAATTGAAACTTGAAACTTGAAAGA GAGCTTCTGAAATTCGAAATTGAAAACTGAAAAACTGAAAGA GAGCTTCTGAAATTCGAAATTGAAAACTGAAAAACTGAAAAG CTTATGGAGGGGAACAATAAAACTGAAAAACTGAAAAACTAAAAA CTTATGGAGGGGAACAATAACAGGATCGAAGAACTGAAAATTGAAAAT LEUGIYGINAlaieuWetSerieuPheValleuNatgeisi	IleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGly 144	ð f	.1769 AsnPheGlyN
CTTATGGGGGGGGAATTGAAAAAA	CTGATTTTCAGCATCATGGGGGTTAACTTGTTTGCGGGAAAGTACCACTACTGCTTTAAT 407	3 6	
CTTATGGGGGGAACAATGGTGAACAATGAAATGGTGAAAAG 4134 CTTATGGGGGGAACAATGGAAGGAACGAGGAACACTTGAAAAG 4134 CTTATGGAGGGAACAATACGAGTGAACAATGAACTTGACAAT 4194 LeuGlyGlnAlaLeuWetSerLeuPheValLeuAlaSerLysAspGlyTrPValAspIle 1491 SIBIT OF TGGGGCAGGATCCTGGCCCTTCTTCAAGTGCAACCTTCAAAGGCTGGATGGA	Glu	දි දි	
CTTATGGGGGAACAATAGGATCAGGAAGAACGTGAAGATTTTGACAAT 4194 CTTATGGGGGAACAATAGGATCAGATGGAAGAACGTGAAGATTTTGACAAT 4194 LeuGlyGlnalaLeuwetSerLeuphevalLeualaSerLysAspGlyTrpValAspIle 1491 S::	GAGACTICTGAAATCCGATTTGAAATTGAAGATGTCAACAATAAAACTGAAAAG 413	ò	1801
Leading of the language of t		qa	5188 AGTGGCTTTA
### STATE CONTRIBUTION OF THE PROPERTY ASSURED CASE AND C		δλ	7
METTYRASPGIyLeuAspAlaValGiyValAspGInGInProlleMetAsnHisAsnPro 1511 ATGTATGCAGTTCCGGAAGCCTGATGAGCCTAAGTATGAGGACATATC 4314 ATGTATGCAGTTCCCGGAAGCCTGATGAGCCTAAGTATGAGGACATATC 4314 TrpMetLeuLeuTyrPhelleSerPheLeuLeulleValAlaPhePheValLeuAsnMet 1531 STACATGTACATCTATTTTTGTCATCTTCATCATCTTCTTCACCCTGAACCTG 4374 PheValGiyValValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluGluGlu 1551 TACATGGTCATCATTGATCACATCAACAAAGAAAGATCGAGGAC 4434 AlaArgArgArgArgTCATCATCAAAAAAAGAAAGATCAGAAAGATCAAAG 4494 AlaArgArgArgArgCluGluLygArgLeuArgArgLeuGluLysLysArgArgLys 1569 ATCTTCATGACAAAAAAAAGAAAAAAGCTGGAGTCAAAG 4494 AlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuValHisHisLeu 1589 AAGCCACAGAAACCCATTCCCGGCCCTTGAAAAAAACTGTCTTTTTTTT		qa	5248 ATCATCATCT
	MetTvrAspGlvLeuAspAlaValGlvValAspGlnGlnProIleMetAsnHisAsnDro 151	ò	m
TrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMet 1531 ::: :::		අු	5308 AGTGTAGCCA
	TrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMet 153	ζ	S
PheValGlyValValValGluAsnPheHisLysCysArgGlnHisGluGluGluGlu 1551		മുവ	68
	PheValGlvValValValGluAsnPheHisLvsCvsArqGlnHisGluGluGluGluGluGlu	ò	1874 TrpProGlyV
AlaArgArgArgIuGluLysArgLeuArgArgLeuGluLysLysArgArgLys 1569 ATCTTCATGACGGAGAACAGAAGTACTACAATGCCATGAAAAAGCTGGGCTCAAAG 4494 AlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeu 1589 AAGCCACAGAAACCCATTCCCCGCCCTTGAACAAATCCTCTTTGATTTT 4554 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuAspLeuPheIleThrGlyValIleGlyLeuAspLeuAspLeuPheIleThrGlyValIleGlyLeuAspLeuAspLeuAspLeuPheIleThrGlyValIleGlyLeuAspLeuAspLeuPheIleThrGlyValIleGlyLeuAspLeuPheIleThrGlyValIleGlyLeuAspLeuPheIleThrGlyValIleUAspLeuAspLeuPheIleThrGlyValIleUAspLeuAspLeuPheIleThrGlyValIleUAspLeuAspLeuPheIleThrGlyValIleUAspLeuAspLeuPheIleThrGlyValIleUAspLeuAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleThrGlyValIleUAspLeuPheIleTh		qa	~
ATCTTCATGACCGAAGAACAACAATACTACAATGCATGAAAAAGCTGGGCTCAAAG 4494 AlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeu 1589 AAGCCACAGAAACCCATTCCCCGCCCCTTGAACAAATCCATGAATTTT 4554 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609 Gy 1932 GTCACTCAGCAAAGCCTTTGACATGATGATGATGATGATGATA 4614	AlaArqArqArqGluGluLvsArqLeuArqArqLeuGluLvsIvsArqArq1vs 156	ζÓ	6
AlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeu 1589	ATCTTCATGACCGAAGAAGAAGAAGTACTACAATGCCATGAAAAAGCTGGGCTCAAAG 449	qu	31 T
	AlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeu 158	δō	914
CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609		අූ	470
Db 5521	CysThrSerHisTyrLeuAspLeuPhelleThrGlyVallleGlyLeuAsnValValThr 160	λō	93
	46	요	521

δγ	1610	MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn ::: :::	1629
Db	4615	- O	4674
٥٨	1630	TyrilePheThrValilePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe	1649
Db	4675	CTGGTGTTTGTTATCTTCTTCACCTGTGAGTGTGTGTCTCAAAATGTTTGCGTTG	4728
٥x	1650	ArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaileValLeuLeuSer	1668
ОЪ	4729	AGGCACTACTACTTCACCATTGGCTGGAACATCTTCGACTTCGTGGTAGTCATCCTCTC	4788
٥y	69,		1688
QQ	4789	Trecease	4842
Οy	1689	IlelleArglleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAla	1708
gg G	4843	CTATTCCGAGTCAFCCGATTGGCCCGTATTGGGCGCATCTTGCGTCTGATCAAAGGCGCC	4902
٥y	1709	ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu	1728
qq	4903		4962
οy	1729		1748
qq	m		5022
٥٨	1749	AspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg	1768
qq	5023		5067
λ̈	.1769		1788
qq	89		5127
δλ	1789		1800
qq	5128 (5187
ογ	1801		1816
qo	5188		5247
λλ	817	ValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeu	1836
qo	5248		5307
λλ	1837 (1853
qq	5308 1		5367
λά	1854 (GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873
qc	5368 (3AGATC	5373
λ'n	1874		1893
qc	5374		5430
λά	1894 /	SerHisPheSerLeuGluHisProThrMetGlnProHis	1913
qc	5431	TTTGCAGATGCCTTGGAGCATCCTCCGAGTGCCAAG	5469
λζ	1914	GlyProAspLeuLeuThrValArgLysSerGlyValSer	1931
ą	5470	CCAAATACCATTGAGCTCATGGCTATGGATCTGCCAATGGTGAGCGGGGAT	5520
λ	1932		1951
qc	5521 (S

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                                                                                          ----TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMe
                                                                                                                                                                                                                                                                                                                        uLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheIl
pserGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePhe---AlaPhePheAl
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                                                  CAGATITIAGTGCCACGCCTGCCTTGTACATTTTAAGTCCTTTTAACCTGATAAGAAGAAT
                                                                        pCysLeuArgThrValCysAsnProTrpPheGluArgIleSerMetLeuValIleLeuLe
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ATE: 2005-10-31
N NUMBER: US 10/482,834
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Sequence 98, Applicat

Sepulication No. US200

GENERAL INFORMATION:

APPLICANT: Wallace,

APPLICANT: Mulley,

APPLICANT: Berkovic

TITLE OF INVENTION:

FILE REFERENCE: 1386

CURRENT APPLICATION NU

PRIOR FILING DATE: 2

PRIOR FILING DATE: 2

PRIOR FILING DATE: 2

PRIOR PELING DATE: 2

PRIOR PELING DATE: 2

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NUMBER OF SEQ ID NOS

SOFTWARE: PATENTIN NU

SEQ ID NO 98
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	CTTTGTGGGTTCTTTCTATCTGGTGAACTTGATCTTGGCTGTGGTGGCCATGGCTTATGA	SerGluThrLysGlnArgGluSerGlnLeuMe ::: :::	**************************************	CATGGAGCAACTTAAGAAGAAGAAGAGGGCAGGCTGCTGCGATGCGCTCTAAGAAGAGGAAGAGGGCAGGTGCTGCGGATGGCCACTTCAGC	oglySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaAr	::: AGGAACTGTCTCAGAAGATGCCATAGAG	gArgLeuAlaGlnValSerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAl	:: GAAGAGGAGGGGGCTC 159	aProLeuGlyGlyGluThrGlnProSerSerSerCysSerArgSerHisArgArgLe	: CCCTCGGAGCTCTTCTGAAATCTCTAAACTCAGGTCAAAGGGAAAGGAAAGGT	uSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisLeuGlyAs	654	nGlyThrLeuArgAlaProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySe	AACAGGAGAAAGAAAGGAAAGCAAAAAGGAACTCTCTGAAGGAGAGAGA	r-ArgArgLeuMetLeuProProProSerThrProAlaLeuSerGlyAlaProProGly-	rcccgagaaggtgtitaagtcagaagatggcagaagatggcatgagaaggaagcttttcggct	GlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisL	GCCAGACAACAGAATAGGGAGGAAATTTTCCATCATGAATCAGTCACTGCTCAG	euGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSerG	CATCCCAGGCTCGCCTTCCTCCCGCCACAACAGCAAGAGCAGCATCTTCAGTTTCAG 188	<pre>lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluT </pre>	GGGACCTGGGGTTCCGAGACCCGGGCTCCGAGAATGAGTTCGC 192	hrbeubysGlubysAlabeuValGluVaiAlaAlaSerSerGlyProProThrbeuThrs 621	<pre>edicaccacacacacacacaacaacaacaacaccacacaca</pre>	:::	hrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGlyA		laCysGlyPro	CTICCEGCCAGCGTGAAGGCGCAACAGCACGGTGGACTGCAACGGCGTGTGTCCCTCAT 213	laGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla- :: ::::: ::: :::	CGGCGGCCCCGGCTCC-CACATCGGCGGGCGTCTCCTGCCAGAGGCTACAACTGAGGTGG 219		AAATTAAGAAGGCCCTGGGATCTCTTTTAGTTTCCATGGACCAATTAGCCTCCTACG 225	SerAspLeuArgAspProH

CCGCCATGCTGGTATAATTTGCCAACACTTTCCTCA 2372 :::|||| -----TACTGGATAAACTGAAAGAGATTGTGA 2417 2537 LystysCysLeuAlaLeuValSerLeuGlyGluHis- 1028 LeuPheAlaLeuGluMetLeuLeuLysLeuLeuValT 797 :::||| ATTTTCACAGCGGAATGTTCCTGAAGCTCATAGCCA 2597 2657 CAGGCCATGTGCTCTTTATGATGTCATGG 3062 3122 |||| |||||::::::::||||:::||||:::||||GAC---GATGGGGAAATGAACAACCTCCAGATCTCAG 3179 AsnLysSerGluSerGluProAspPhePheSerProS 1009 ||||||| :::|||| | AAGAAGGGTGTGGCCTGGACCAAACTAAAGGTGCACG 3227 2717 ::: CTGGGCAACCTGACACTGGTGCTGGCCATTATTGTCT 2837 CAACTCTTTGGAAAAGCTACAAAGAGTGTGTCTGCA 2897 CAGCGTGAGGCTGATGAGGCTCTGGATGAGT 3287 ValleuAlaPheTrpArgLeuIleCysAspThrPheA 737 777 837 877 890 AsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 969 ValArgPheLeuProAlaLeuGlnArgGlnLeuValV 857 SerSerTrpAlaAlaLeuTyrPhelleAlaLeuMetT 949 ValAlaThrPheCysMetLeuLeuMetLeuPheIleP HisGluGlnProGluGluLeuThrAsnAlaLeuGluI GlnIleLeuThrGlnGluAspTrpAsnLysValLeuT AspAlaSerGlyGlnLeuSerCysIleGlnLeuProV uProProLeuIleIle-----HisLeuPheGly-----

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uLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728 uLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGly 1748 1589 1649 1668 5020 1708 1569 4672 4732 1609 4792 rGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn 1629 4966 4552 TGATAACTTCAATCAACAAAAAAAAAGTTCGGAGGTCAGGAC 4612 oAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPro 1511 iglyvalGlnLeuPheLysGlyLysPhePheValCysGlnGly 1443 1471 LSerieuPheValLeuAjaSerLysAspGjyTrpValAspJje 1491 ||||| :::|||| :::|||| || ::: epheValLeuGluSerValPheLysLeuValAlaPheGlyPhe gValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAla rTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeu TCCCCGCCCCTTGAACAAATCCAAGGAATCGTCTTTGATTTT nAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSer uGluGluIjeGluValAsnAlaSerLeuProIleAsnProThr |::: TTCCCGGAAGCCTGATGAGCAGCCTAAGTATGAGGACAATATC elleSerPheLeuLeulleValAlaPhePheValLeuAsnMet lGluAsnPheHisLysCysArgGlnHisGlnGluGluGluGlu u-----LysArgLeuArgArgLeuGluLysLysArgArgLys ACAGAAGAAGTACTACAATGCCATGAAAAAGCTGGGCTCAAAG uAspLeuPhelleThrGlyVallleGlyLeuAsnValValThr ||||| :::||||||| :::|||||| AGAGGGATGAGGGTGGTGGTGAAT ıLysProjleGlyAşnıleValValIleÇysCysAlaPhePhe -AlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsn :|||||| 3GGAGTTAACTTGTTTGCGGGAAAGTACCACTACTGCTTTAAT

RESULT 15 US-11-263	Publicat ; GENERAL ; APPLICA	; APPLICA	; FILE RI ; CURRENT ; CURRENT	PRIOR A PRIOR A PRIOR A	; PRIOR ; PRIOR ;	; NUMBER ; SOFTWAE	; SEQ ID N ; LENGTH ; TYPE: ; ORGANI	7	Alignment Pred. No.:	score: Percent Si Best Local	Query Mato DB:	US-09-611-	ò f	B &	Š &	\ \frac{1}{2}	g 2	₹ 6 	ò	გე .	λος O	λō	qa	රු යි	λό qa	
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Matches:
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DÞ	850 ACTGAGGGCTTTGAAAACTATTTCGGTAATCCCAGGCCTGAAGACAATTGTGGGTGCCTT 909	ò	'
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DÞ	910 GATTCAGTCTGTGAAGAAACTGTCAGATGTGATCCTGACAGTGTTCTGCCTGAGTGT 969	ò	563 euGlı
ò	ePheGly11eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeu 243	qa	1825 CATC
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δδ	rCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyGlyProProCysGl	q _O	1983
da	TTTCTACACAGTTCCT	λõ	641 hrGly
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qq	1243 TITTAGCIGGGCCTICTIGGCATIATTICGCCTTAIGACCCAGGACTATIGGGAAAACTI 1302	δ 	669
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Op	1303 GTATCAATTGACTTTACGAĞCAGCCGGGAAAACATACATGATCTTCTTCGTCTTGGTCAT 1362	δŏ	703
δ	379 ellevalGlySerPhePheMetlleAsnLeuCysLeuValVallleAlaThrGlnPhe 398	QC	2253 GGCG
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ò	aProLeuGlyGlyGluThrGlnProSerSerSerCysSerArgSerHisArgArgLe 48	qq	:: 2538 TAGG
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	r-ArgargieuMetleuProProSerThrProAlaLeuSerGlyAlaProProGly- 548		GCCAGACAACAGAATAGGGAGGAAATTTTCCATCATGAATCAGTĊAĊ'TĠĊTCAG 1824	50	rcrrcagrrrcag 1	JyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluT	GGGACCTGGGCGGTTCCGAGACCCGGGCTCCGAGAATGAGTTCG	hrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThrS 621	GGATGACGAGCACAGCACGGTGGAGGAGGGAGGGCCGCCGGGGACTCCCTCT 19	ਮੁ	100 C100C00C00	hrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGlyA b61	CAGCGGCTACAGCGGCTACAGCCAGGCAGCCGCTCTCGCGCATCTTCCCAG &	A 67	ccirccicacaecergaaececaacaecaceceregacrecaaceceregrer	laGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla- 692	CGGCGGCCCCGGCTCC-CACATCGGCGGGCGTCTCCTGCCAGAGGCTACAACTGAGGTGG		AAATTAAGAAGAAAGGCCCTGGATCTCTTTTAGTTTCCATGGACCAATTAGCCTCCTACG		GGCGGAAGGACAGAATCAACAGTATAATGAGTGTTGTTACAAATACAĞTAGTAGAAGAAC 2312	isSerArgArgGlnArgSerLeuGlyPro	TGGAAGAGTCTCAGAGAAAGTGCCCGCCATGCTGGTATAAATTTGCCAACACTTTCCTCA 2372	AspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheA 737	; TCTGGGAGTGCCACCCCTACTGGATAAAACTGAAAGAGATTGTGA 2417	rgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnT 7	ACTTGATAGTTATGGACCCTTTTGTGGATTTAGCCATCACCATCTGCATCGTCCTGAATA 2		cactgitiaiggcaatggagcaccatcaagacaccacaattigaacatgitiggcig 2537	leSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLys	<u> raggaaatcregittrcactggaatritcacagcggaaattcctgaagcreatagcca</u>	17	9 9	7 leservaltrpglullevalglyglnglnglyglyglyLeuservalLeuArgThrPheA 837 :: ::: :::
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qq	3620	GTGGAA 3625
δλ	1214 ProAspAspProProLeuAspGlyAspAspAla	ProLeuAspGlyAspAspAlaAspAspGluGly 1228
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QQ	3914 GAGATGTTGCTCAAGTGGACAGCCTATGGCTTG	CAAGTT
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δγ	serAspSer	GlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeu 1383
Dp	4022 AATGCCCTGGCTACTCGGAACT	sdigccaraaagrcciraadacccra 4072
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пр	4133 GCCTTGGTGGGGGCCATCCCCTCCATCATGAA	srecrecrearerercrearcrande 4192
ò	1424 IleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGly	JysGlyLysPhePheValCysGlnGly 1443
qq	4193 CTGATTTTCAGCATCATGGGAGTTAACTTGTT	scedelalaccactactectraat 4252
٥٨	1444 GluAspThrArgAsi	145
qq	ğ	stcaacaataaactgaatgtgaaaag 4312
ò	1458AlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsn	147
Dþ	4313 CTTATGGAGGGGAACAATACAGAGATCAGATG	aagaacgigaagaicaactitigacaat 4372
ò	1472 LeuGlyGlnAlaLeuMetSerLeuPheValLe	ValLeuAlaSerLysAspGlyTrpValAspIle 1491
QQ	4373 GTTGGGCAGGATACCTGGCCCTTCTTCAAGT	TGGACAT
۵,	1492 MetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnFrolleMetAsnHisAsnFr	SlnGlnProlleMetAsnHisAsnPro Sl
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0y 1	TrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMet 15
7	
. 4	1532 PhevalGlyvalValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluL 1551 ::: 4553 TTCATTGGTGTCATTGATAACTTCAATCAACAAAAGAAAAAGTTCGGAGGTCAGGAC 4612
	AlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgLys
4.	
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., 4	1590 CysThrSerHisTyrLeuAspLeuPhelleThrGlyVallleGlyLeuAsnValThr 1609
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.7	1630 TyrilepheThrValilePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe 1649
4	4853 CTGGTGTTTGTTATCTTCTTCACCTGTGAGTGTCTCAAAATGTTTGCGTTG 4906
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4	1669 IlemetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThr 1688
, 1	1689 IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAla 1708
	sozi craficcadeccicalificaccicalificaccicalificaticalicalical soso
	1709 ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728
	5081 AAAĠĠĠĀŢĪĊĠŤĄCCĊŢĠĊŤĊŢŢŢĠCĊŢŢĠĠĊŢĠĊĊŢĠĊĊŢĠĊŢĠĊŢĠĠĀĊĄŢĊ 5140
u	1729 GlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGly 1748
•	
, - 1	1749 AspLeuGlucysAspGluThrHisProcysGluGiyLeuGiyArgHisAlaThrPheArg 1768
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	1854 GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu 1873

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SerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGln 2065
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|-----GAGCCAATCACAACCACACTGCGAGCAGCAGGAGGAGGTATCT 5872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis 1913
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| S552 TGGGAGAAGTTCGAC---CCCGATGCCACCCAGTTCATTGAGTACTGTAAGCTGGCAGAC 5608
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; Sequence 3, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
; TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
; FILE REFERENCE: ORT-1057
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 3
; LENGTH: 6822
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      aAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln
CTGCCAGGACCAGACTTACTGACTGTGCGGAAGTCTGGGGTCAGCCGAACG
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OF DETECTION AND 110 US-09-611-257A-37 (1-2266) x US-09-949-016-3859 (1-7405) GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-00-10-20
PRIOR PPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3859
LENGTH: 7405
TYPE: DNA
US-09-949-016-3859 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 0 11241.00 95.1% 95.1% 94.4% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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LeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhe

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RESULT 3 US-09-949-016-3859 ; Sequence 3859, Application US/09949016

pGluAlaLeuLysIleCysAsnTyrIlePhe 1LysProlleGlyAsnIleValVallleCys ThrashlysSeraspcysAlaGluAlaSer JG1UG1UA1AArgArgArgG1UG1ULYSArg -----LysAlaGlnCys AlalleValLeuLeuSerIleMetGlyIle LeuThrLeuSerAsnTyrllePheThrAla GlyThrLysIleLeuGlyMetLeuArgVal JG1yValG1nLeuPheLySG1yLySPhePhe

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yThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLys
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                                             AlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSer
                                                                            HisSerLys1leSerLysHisMetThrProProAlaProCysProGlyProGluProAsn
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TrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrp
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Batent No. 678393;

Patent No. 678393;

GENERAL INFORMATION:

APPLICANT: Issa, Jean-Pierre

TITLE OF INVENTION: CACNAIG POLYNUCLEOTIDE POLYPEPTIDE AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: JHU1590

CURRENT APPLICATION NUMBER: US/09/398,522

CURRENT FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 120

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 51

LENGTH: 3993
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NAME/KEY: CDS
LOCATION: (373)...(3993)
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Matches:
Conservative:
Mismatches:
Indels:
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                                     COPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 249...7307

OTHER INFORMATION:

US-08-984-709A-49
  TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 49
SEQUENCE CHARACTERISTICS:
LENGTH: 7898 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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CAGTGGCGCTGGAGCAG 3667 ohisarghisargGlyse 1163 ACTGCGGCGGCCGAGTC 3841 rAlaSerGlyArgGlySe 1192 rgacacccrccrcaga 3961 oGluGlyAsnLeuSerLy 1232 GluAlaLeuGlyProAl 1065 AGCCCCCAGCCTCCCAGA 3553 CAAGTGCCGCGATCGCGA 3901 SerLeuAspGlyAsp-- 1013 ::: |||| |CACTTCGAGGAGGACTT 3373 LeuAlaLeuValSerLe 1025 ::: ||| |CTGGGAGACCAGAAGCC 3607 AlagluGluIleSerLy 974 994 ThrPheGlyAsnTyrVa 99-----)ValAspSerGlnGlyGl rren----naga


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Sequence 1, Application US/09404650

Sequence 1, Application US/09404650

Patent No. 6309858

APPLICANT: Dietrich, Paul S.
APPLICANT: Dietrich, Paul S.
APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: T-TYPE Sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650

CURRENT FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO

SEQ ID NO

CRGANISM: Homo sapiens

FEATURE:

NOMME/KEY: CDS

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NOMME/KEY: CDS
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1837	uGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMe 185	à à
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~	yValGluGlyProAspSerProAsp 18	à i
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	582 GCAAGAGGTGCAGCTGAGACGGAGGCCTTCTCCCTGAACTCAGACAGGTCCTCGTC 5641	ò

~ 0	1901 rHisPheSerLeuGluHisProThrMe 	rMetGlnPro 1912
> 0	1913HisProThrGluLeuProGlyProAspLeuLeuThrValArgLy	rValArgLysSerGly 1929 TGTGGGAGACCTGGGCGAATG 5761
> 0	ValSerArgThrHisSerL ::: cTTCCCTTGTCCTCTACGGCCGTCT	euProAsnAspSerTyrMetCysArgHi 1945 ::: :::::::: cgcccGaTcCAGAGAACTTCCTGTGTGAGAT 5821
> 0	sGlySerThrAlaGluGlyProLeuGlyH :: GGAGGAGATCCCATTCAACCCTGTC	pGlyLeuProLysAlaGlnSe 1965
	965 rGlySerValLeuSerValHisSerGlnProAlaAs	pThrSerTyrIleLeuGlnLeuPr 1985 ::: :::
	o ro	aProTh 199
0	30	 AGGCCCAGAAAAGGGCACTGG 5989
> (1999 rTrpGlyThrlleProLysLeuProProProGlyArgSel	CTRAGGCATCTCTGCGGTCACCAAG 6049
· ~	014 uAlaGlnArgPr	alGlnGl 203
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>	euGlySerArgGl	SerGlyProSerProProLeuAlaAr 2054
Ω	6102GCCA	ccccadcagcrccgcggcag 6127
ء. ح	PheTracect	nGlnHisSerArgSerHisSe 2074 ::: ::: CAGCCCCGGCGTGCC 6182
· >-	074 rLysIleSerLysHi	nTrpGl 2
0	1 1 1 1 1 1	 AGGACCCCGGCCGGCTGTC 6226
>-	ysGlyProProGl	erTrpileSe 211
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م د	euProProGlyGly	roProSerProArgAspLeuLysLy 2134
· >-	134 sCysTyrSerValGluAlaGlnSerCysGlnArgA	SerTrpLeuAspGluGl 2
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>-	leAlaValSerCysLeuAspS 	GlnProHisLeuGlyT
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a >	191 oLvsLvsLvsLeuSerProProSerIleThr	rGl 220
, <u>a</u>	416 CTCGGAGACCCTCAGCAGCCTCTCGCTCACCTCCCT	CTGCCGCCCC 64
>	GlyProArgThrProProSerProGlyIleCysLeuA	ArgArgArgAlaProSerSerAs 2228
д	468ccgcccccccccccccccccc	ZAGGAAGTTCAGCAGCAG 65
>		coProAspSerMetAlaAlaSe 2244

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Sequence 1, Application US/09935541

Batent No. 6589787

GENERAL INFORMATION:

APPLICANT: Dietrich, Paul S.

APPLICANT: McGivern, Joseph G.

TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

TITLE OF INVENTION: AND USES

FILE REFERENCE: R0043B-REG sequence listing

CURRENT APPLICATION NUMBER: US/09/935,541

CURRENT FILING DATE: 2001-08-23

PRIOR FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 1

LENGTH: 6816

TYPE: DNA

COGGANISM: Homo sapiens

FEATURE:

SEAUTH: 6816

TYPE: DNA

FEATURE:

SEAUTH: 6816

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udsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIl |||||||||||||||||| |CAACGTGGTCACCATGTCCCTGGAGCACTACAATCAGCCCACGTC uLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe||||||||||||||||||::cAaGTACTGCAACTATATGTTCACCACTGTCTTTGTGCTGGAGGC uLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGl |||||||||||| |GCTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGTGCGAGGG aThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa |||||||| |cacctrcGaGaACTTCGGCATGGCCTTCCTCACACTCTTCCAGGT rProGlnProHisSerProLeuGlySerProPheLeuTrpProGl :::||| ccaggactccttggagggggggctgaccatcatcgacaacctgtc **AGGGGGGGGGGGGGGGACACCGAGGGCGGCTTGTGCCGGCG** sProGlyAlaLeu--pSerProAsp-

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Sequence 1, Application US/10425800

Patent No. 6893842

GENERAL, INFORMATION:

GENERAL, INFORMATION:

APPLICANT: Dietrich, Paul S.

APPLICANT: McGivern, Joseph G.

TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

TITLE OF INVENTION: AND USES

FILE REFERENCE: R0043B-REG sequence listing

CURRENT APPLICATION NUMBER: US/10/425,800

CURRENT FILING DATE: 2003-04-29

PRIOR FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 6816
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; Sequence 3, Application; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich,
; TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: CURRENT FILING DATE:
; NUMBER OF SEQ ID NOS:
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659 SerGlyAlaCyeGlyProAspSerCyrCyeAlaArg			1 5
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693 ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPrOHisSerArgArg 712 1836 GGTGGCGAGGACGAGGCGGATGGGGCCCGGAGCGGGGCC 1889 713 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu	TCGGGCCTGGGCAGCACCGAC	18	10 00
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765 HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784	2010 TTCAACCGGGCATCATGATGGCCATCCT	20	2970
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	1520 eLeuLeulleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh	560 uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe 158	508 TCACACCCGGCTGCTCCATCTCCATGTGCACCACCTACCT	uAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGl :::		AlaSerLeuProlleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaA					817 lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGl 183 228 GCTCACCGCGCAGTTCGTGCTCATCAACGTGGTGGTGGTGCTCTGTGTTGAAGCACCTGGA 528 837 uGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluLeuGluMe 185 ::::
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ò	805 AsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGly 824	; <u>අ</u>	3132 CGGTCTGCGAGG
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WENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

WENTION: AND USES

NCE: R0043B-REG sequence listing

LICATION NUMBER: US/10/425,800

LING DATE: 2003-04-29

CATION NUMBER: US/09/404,650

G DATE: 1999-09-23

EQ ID NOS: 12
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Batent No. 6893842

GENERAL INFORMATION:

APPLICANT: Dietrich, I

APPLICANT: McGivern,

TITLE OF INVENTION: T-

TITLE OF INVENTION: P

FILE REFERENCE: R0043E

CURRENT APPLICATION NU

CURRENT FILING DATE:

PRIOR PILING DATE:

PRIOR PILING DATE:

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS:

SOFTWARE: PatentIN Ver
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Sequence 12, Application US/09404650

Sequence 12, Application US/09404650

Patent No. 6309858

GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650

CURRENT FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 6503
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Sequence 12, Application US/09935541

Patent No. 6589787

GENERAL INFORMATION:

APPLICANT: Dietrich, Paul S.

TILE OF INVENTION: T-TYPE CALCIUM CHANNEL VAR:

TILE OF INVENTION: AND USES

FILE REFERENCE: R0043B-REG sequence listing

CURRENT APPLICATION NUMBER: US/09/935,541

CURRENT APPLICATION NUMBER: 09/404,650

PRIOR APPLICATION NUMBER: 09/404,650

PRIOR FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 6503

TYPE: DNA

CORGANISM: Rattus SP.

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Sequence 12, Application US/10425800

Sequence 12, Application US/10425800

Patent NO. 6893842

GENERAL INFORMATION:

APPLICANT: Dietrich, Paul S.

APPLICANT: McGivern, Joseph G.

TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

TITLE OF INVENTION: AND USES

TITLE REFERENCE: R00438-REG sequence listing

CURRENT APPLICATION NUMBER: US/10/425,800

CURRENT APPLICATION NUMBER: US/09/404,650

PRIOR APPLICATION NUMBER: US/09/404,650

PRIOR FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 6503
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AGCACCCCAGAGCCCTTTCTCCCCGGATGGCTCCAGCCCCTCTCTTAGATGCCTGAAA
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                          uArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-
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3004 GTCCCTGGGCAGGATGAGCTATGATCAGCGATCCTTGTCCAGCTCCCGGAGCT	 	α (57
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Ωp	13204 ATTITICAACCCCTCCAGIGAICCIAACTIGCAGIGAAAITIGAAAAICACTATICCAG 13263	ò	380
ò	249 249	7 A	14343 ATACCACCTCTCCCAGAGGGCATTTGGAAATGGGAAAGGGTGATTCTGGTTTTTGATTTTT 14402
qa	13264 GATGTGACCTTCCAACATCCTGAGTCTGGAGTTTCCCCACTCAGGCCTCATGCTCCTGGT 13323	ò	
δ	9 249	qq	14403 ITTAATAGCTTTATTGAGACATAACTCACATATCATTCAATTCATCCTTTGAATGAA
qq	บ บ	δλ	380 380
δλ	249	qa	14463 CAGTGGTTTTTTAAGCATGTTTACAGAGTTCTGTTTTTTTT
qa	13	ον	380
ò		අු	14523 ATTGGCAATTTGTTACTGGGGGGGGGGGGGGAGAGCTAAAACATCCTGAAATGCTTGCAAAT 14582
qq	CTCCCCAGTCTCACCCCTGTTCCCCTTCCCATCCTGCAGCCCCTGAGCGTGGACCTGGA 13	ολ	380
ð 1	uArgTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGl 276	qa	14583 AAAGAATTATTCTACCCAAAATTCTGATCAGTGATCAATTGGTGTTAAATGCTGCCTGAT 14642
අධ	GCGCTATTACCAGACAGAGAGGAGGATGAGAGCCCCTTCATCTGCTCCCAGCCAG	λΌ	380
<i>ਨ</i> ਹ		qa	14643 CTCTTATTCCTGCCAGTTCAGAAATTGCCAGACTTTAAGAAGGCAGAAGACGGAGGCAAA 14702
a	GAACGGCATGCGGTCCTGCAGAAGCGTGCCCACGCTGCGGGGGGGG	δλ	380
රු සි	296 OProCysGlyLeuAsDTyrGluAlaTyrAsnSerSerSerAsmInrInrCysValAsmII 316 [qa	14703 AGCAGCAATATTTAATAGTTTTAATCACTACCATTCATAGTTAATAACTTCATCGCCACC 14762
3 6	22 A C C C C C C C C C C C C C C C C C C	δγ	380
Š 1	DASNGINIYIIYIINIASNCYSSEIAIGGIYGIUAISASNKIOKNEUVSGIYALGILEAAS	qu	14763 ACTITGAGCTAATATTTATTGAGCACTTACTATGCGCCCAGCCCCTGATCTAAGCACTTTC 14822
an i	GAACCAGIACIACAACIGCICAGGGGGGGGGGGCACACCCCIICAAGGGGGGGCGCCAICAA IS /4	δλ	380
Š i	336 nPheAspAsniieGlyTyrAtairplieAlaliePheGli 349	qα	14823 AATGTGCTGGTGCATTTAATCCTCACCGTGATCCTCTCCATTTTACAGATGAGGAAACTG 14882
g O	CTTTGACAACATTGGCTATGCCTGGATCGCCATCTTCCAGGTGGGGCAGCCTGGGCCCCG	ò	380
à i	34.9	qq	14883 ACATTTCCTCATTTATCTGACCCTACCAGACGCTTTGCCTATGCTGTGTATTAATCTCCA 14942
qq	GGAGCTTCCCCAGAACACCCCCAGGACACAGCCCCAGGATCGGAGGGTCGCTCTCAG 13	δ	380380
È	34.9	Ωp	14943 AGAGTGGGGCATCACTGCTGACGTATGCTGTAACATCTGCTGCCTGTTTAATCCTCGTCG 15002
අු	GGTTGGGGGTGGGGGCCTCTGGAGGAGACTGAAGGAGATTTGGTGGGCCCATAG 1	ò	380
ò		qq	15003 ICCCCTGTGAGGTGCCAGGGCAGGGATTGTGGTCCCCATCTTAAATGAGAATTCAGCG 15062
qq	TCAGCCTGCCCTCTGCACCCCCTAGGTCATCACGCTGGAGGGCTGGGTCGACATCATGT 13	ò	380
ò	yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeulleIle-380	qq	15063 CCCCAGAGGGTGGGTCACTGGGCCAAGATCACACAGAAAGTAAGCGGCTGGGGCTGAGAA 15122
QQ	13984 ACTTTGTGATGGATGCTCATTCCTTCTACAATTTCATCTACTTCATCCTCCTCATCA	ò	380

8	179	Qy 641	641
ÿ å		Db 18423 TG	GTGTGTGTGCGTGTGCATGTGTGTGTGTTCATATGCATATGTGTGCACATGT 18482
<u> </u>	GGACCAGGGCITAIAIICICAIGCICCICAIGGCITAGGCACCIICAACCAGICACA	Qy 641	641
ò	641	Db 18483 GC	TTGATGTGTG
qq	17403 TCCCTGCTATGAGCTCGAATTTTCTCATCTGCTAAAGTGGAACTCATAATTCCTACATTG 17462	641	4
ò	641 641		~^^
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ò	641 641	Oy 641	641
ପ୍ର	CAACTGTTGCACACACAATGGCTGTGTGCCTGTCACATGCTTTGCGGGCAAAATTCCAT	Db 18603 TG	CATGTATGTGCCCATATGGTGGTGTCCAAATAGTATACATGTGTACACGAGTGTGC 18
ઠે		Оу 641	
; a	TGGATCCTCTCTACCCATTAAGTGATAGGCTTTCTTAGCATCCCCATTGTGGATGAGA	Db 18663 GC	TCTGGAGCACGTGTGCAGGTGCACGTGTCTGGTGTGGGGTGTGTGT
8		Oy 641	
i 2		Db 18723 GT	GTGGGCGTGTCTTAAGGATCCCATGGAAAGTGCTGCTCA
3 8		Oy 641	641
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3 8	0//T)	Qy 641	1 1 1 1
ò	1.4.1	Α 3	CTGTCCAGGACCTCAGAGGACATCCAGGCCACCTCTCTGAGCCCC
යු	17763 TGTGCCCAGCTTCATGCCCCACTGGCTAAACCTGAGTCTCATTGCCTCCGCACAGGGAGA 17822	641	
ò	641 641	Db 18903 GT	GACTGTCAATGAAGTGCTATTGACATTAGGGCCATCTTGTGGGTCAAGACTGCCCACC
qa	17823 CCCAGTTCAGGGAGCTGCTTGTCTGATGGGTGACACTCCCAGTGTGGGGGGCAGTGAG 17882	641	641
ò	641 641		0. 10 4 40 4 40 40 40 40 40 40 50 50 40 50 40 50 50 50 50 50 50 50 50 50 50 50 50 50
QQ	17883 ACACATAGGGACGTCGGGCTCTCCCCAGCAGACAGGTTCACTGTAGCTGCAGGCCCACGGC 17942	T 8863 T	CIGACAIICAGCACCCCIGGCCCCACIAAGIGCCIAGCACCCCAICACIGIAACAACC IAOS
δ	641 641	641 -	T600
QQ	17943 CTGTGTTTCAGGAAGGATGTGGCACGTGGGGAGCGGGATATTCGTGGGGATGTTACG 18002	19023 C	ACTCCCTGACTCTTTACACATACTCACAGGGCAGGGTAGCCCCAGGTACGAGAC 19
ò	641 641	642	
qq	18003 TGGGAATGTGGGCTGGGACCAGAAGGTGCTATCACAGAACCCCAGAGGGTTTCTAT 18062	19083 T	rrgcaagarc 19
ò	641 641	651 8	70
QQ	18063 GCCAGCTCCTCCACTACCCTGCCACGGACGTGGGCCAGTCACATGCACCCACGTTTTTA 18122	19143 T	cecellaciel i
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ò	641 641	7 6 6	
qq	18363 IGTGCGCACGAGTGCATCTAGTATGCGTGTATGCGTCTATGTCCATGAAGGGGTCCAGTG 18422	177	uThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMet 790

	791 LeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePhe 810
	19536 CGCCTGGGGGCTGGGGCCTTCTACCTCCCTCGCACCCCTCCTGAGCTC 19586
	811 AspGlyValIleValValIleSer-ValTrpGluIleValGlyGlnGlnGlyGlyGlyLe 830
	19587 AGCTTCCTCCATGCTGCTAGCCCACCTGGCAGGTAGGAGGGGAGGTGGTGGATGGA
	830 uSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPhe 847
	19645GCAATGCATGGGGATTCTCTAGAGGGAGTGCTTAAAGTCTCTGAGTATGGAGGTCG 19700
	848
	19701 CCTCAGGTAGGCCACAGGGTATGTTCTACCCAGGAAGGCTGCTCAGAGGAGGCTGTTT 19760
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